

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2005, 18:05:25 ; Search time 109.109 Seconds
(without alignments)
3214.888 Million cell updates/sec

Title: US-09-591-632-2
Perfect score: 3594
Sequence: 1 MDSNQNNQNYQYQSQNG.....FTLRDQGTIAIGKIVKIAE 685

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3594	100.0	685	1 ERF2_YEAST	P05453 saccharomyc
2	3590	99.9	685	2 Q9HGV1	Q9HGV1 saccharomyc
3	3587	99.8	685	2 Q8TFB8	Q8TFB8 saccharomyc
4	3455.5	96.1	666	2 Q8TFR7	Q8TFR7 saccharomyc
5	3450.5	96.0	666	2 Q8TFR8	Q8TFR8 saccharomyc
6	2632.5	73.2	688	2 Q8FVM2	Q8FVM2 candida gla
7	2549.5	70.9	662	2 Q9HG14	Q9HG14 zygosacchar
8	2471	68.8	700	2 Q8CQF8	Q8CQF8 kluyveromyc
9	2471	68.8	700	2 Q9HG18	Q9HG18 kluyveromyc
10	2464	68.6	691	2 Q750T4	Q750T4 ashbya goss
11	2367	65.9	712	2 Q9HG17	Q9HG17 candida mal
12	2345.5	65.3	715	1 ERF2_CANAL	O13354 candida alb
13	2303	64.1	435	2 Q6Q7I3	Q6Q7I3 saccharomyc
14	2296	63.9	435	2 Q6Q7I6	Q6Q7I6 saccharomyc
15	2287	63.6	435	2 Q6Q7I2	Q6Q7I2 saccharomyc
16	2283.5	63.5	701	2 Q9HG16	Q9HG16 debaryomyc
17	2281	63.5	435	2 Q6Q7I4	Q6Q7I4 saccharomyc
18	2277.5	63.4	701	2 Q8BWQ4	Q8BWQ4 debaryomyc
19	2274	63.3	429	2 Q96UJ2	Q96UJ2 saccharomyc
20	2272	63.2	435	2 Q6Q7I1	Q6Q7I1 saccharomyc
21	2267	63.1	429	2 Q96TJ4	Q96TJ4 saccharomyc
22	2263	63.0	429	2 Q96UI9	Q96UI9 saccharomyc
23	2257	62.8	429	2 Q96UJ1	Q96UJ1 saccharomyc
24	2253	62.7	429	2 Q96UJ0	Q96UJ0 saccharomyc
25	2249	62.6	429	2 Q96U18	Q96U18 saccharomyc
26	2243	62.4	429	2 Q96TQ9	Q96TQ9 saccharomyc
27	2178	60.6	434	2 Q96UJ3	Q96UJ3 saccharomyc
28	2177	60.6	741	1 ERF2_PICPI	P23637 pichia pinu
29	1877	52.2	742	2 Q9HG15	Q9HG15 yarrowia li
30	1855	51.6	728	2 Q8CFC9	Q8CFC9 yarrowia li
31	1721	47.9	730	2 Q7S6P5	Q7S6P5 neurospora

RESULT 1					
ID	ERF2_YEAST	STANDARD;	PRT;	685 AA.	
AC	P05453; P05420;				
DT	01-NOV-1988 (Rel. 09, Created)				
DT	01-NOV-1988 (Rel. 09, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DE	Eukaryotic peptide chain release factor GTP-binding subunit (ERF2)				
DE	(Translation release factor 3) (ERF3) (ERF-3) (Omnipotent suppressor protein 2) (G1 to S phase transition protein 1).				
DE	Name=SUP35; Synonyms=GST1, PNM2, SAL3, SUP12, SUP2;				
GN	OrderedLocustNames=YDR172W; ORFNames=YD9395.05;				
OS	Saccharomyces cerevisiae (Baker's Yeast).				
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;				
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.				
OX	NCBI_TaxID=4932;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=88329727; PubMed=3047009; DOI=10.1016/0378-1119(88)90223-5;				
RA	Kushnirov V.V., Ter-Avanesyan M.D., Telckov M.V., Surguchov A.P.,				
RA	Smirnov V.N., Inge-Vechtomov S.G.;				
RT	"Nucleotide sequence of the SUP2 (SUP35) gene of Saccharomyces cerevisiae."				
RT	Gene 56:45-54 (1988).				
RL	[2]				
RN	SEQUENCE FROM N.A.				
RP	MEDLINE=87213095; PubMed=3556215; DOI=10.1016/0014-5793(87)80157-6;				
RX	Kushnirov V.V., Ter-Avanesyan M.D., Surguchov A.P., Smirnov V.N.,				
RA	Inge-Vechtomov S.G.;				
RA	"Localization of possible functional domains in sup2 gene product of the yeast Saccharomyces cerevisiae."				
RT	FEBS Lett. 215:257-260(1987).				
RL	[3]				
RN	SEQUENCE FROM N.A.				
RP	MEDLINE=88172503; PubMed=3280807;				
RX	Wilson P.G., Culbertson M.N.;				
RA	"SUF12 suppressor protein of yeast. A fusion protein related to the EF-1 family of elongation factors."				
RT	J. Mol. Biol. 199:559-573(1988).				
RL	[4]				
RN	SEQUENCE FROM N.A.				
RP	MEDLINE=88296422; PubMed=2841115;				
RX	Kukuchi Y., Shinatake H., Kikuchi A.;				
RA	"A yeast gene required for the G1-to-S transition encodes a protein containing an A-kinase target site and GTPase domain."				
RT	EMBO J. 7:1175-1182(1988).				
RL	[5]				
RN	SEQUENCE FROM N.A.				
RP	STRAIN=S288c / AB972;				
RX	MEDLINE=97313263; PubMed=9169867;				
RA	Jacq C., Alt-Moerbe J., Andre B., Arnold W., Ballesta J.P.G.,				
RA	Bargues M., Baron L., Becker A., Biteau N., Bloeker H., Blugeon C.,				
RA	Boskovic J., Brandt P., Brueckner M., Buittago M.J., Coster F.,				
RA	Delavaeu T., del Rey F., Dujon B., Eide L.G., Garcia-Cantalejo J.M.,				

32	1714	47.7	716	2	O42787	O42787 podospora a
33	1689	47.0	662	1	ERF2_SCHPO	Q74718 schizosacch
34	1626	45.2	629	2	Q96WS7	Q96WS7 pneumocysti
35	1377	38.3	633	2	Q96GF2	Q96GF2 homo sapien
36	1375	38.3	614	2	Q91855	Q91855 xenopus lae
37	1364	38.0	498	2	Q7KZX8	Q7KZX8 homo sapien
38	1359.5	37.8	553	2	Q6DD07	Q6DD07 xenopus lae
39	1357	37.8	587	2	Q8K2E1	Q8K2E1 mus musculu
40	1354.5	37.7	499	1	GSP1_HUMAN	P15170 homo sapien
41	1353.5	37.7	588	2	Q9N2G7	Q9N2G7 oryctolagus
42	1353.5	37.7	636	2	Q6AYD5	Q6AYD5 rattus norv
43	1352	37.6	498	2	Q8CCV1	Q8CCV1 mus musculu
44	1346.5	37.5	597	2	O88180	O88180 mus musculu
45	1346.5	37.5	628	2	Q9NY44	Q9NY44 homo sapien

ALIGNMENTS


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QY 301 DAGRGWYLSWVMDTNKEERNDGKTIIEVGKAYFETEKRRYTILDPAGHKMYVSEMIIGAS 360
DB 301 DAGRGWYLSWVMDTNKEERNDGKTIIEVGKAYFETEKRRYTILDPAGHKMYVSEMIIGAS 360
QY 361 QADVGVLLVLSARKGEYETGFERGGQTRHALLAKTQGVNKMVWVVKMDPTVWNSKERY 420
DB 361 QADVGVLLVLSARKGEYETGFERGGQTRHALLAKTQGVNKMVWVVKMDPTVWNSKERY 420
QY 421 DQCVSNVSNFLRAIGYNIKTDDVMPVSGYSGANLKDHDVDPKPCPWTGPTLLEYLDTMN 480
DB 421 DQCVSNVSNFLRAIGYNIKTDDVMPVSGYSGANLKDHDVDPKPCPWTGPTLLEYLDTMN 480
QY 481 HVDRHINAPFMLPIAAKMKDLGTTVEGKIESGHIKKGSTLLMPNKTAVEIQNIYNEN 540
DB 481 HVDRHINAPFMLPIAAKMKDLGTTVEGKIESGHIKKGSTLLMPNKTAVEIQNIYNEN 540
QY 541 EVDNMCGEQVKLRIGVEBEDISPGFVLTSPPKPIKSVTKFVAQIAIIVELKSIIAAGFS 600
DB 541 EVDNMCGEQVKLRIGVEBEDISPGFVLTSPPKPIKSVTKFVAQIAIIVELKSIIAAGFS 600
QY 601 CVMHVHTAIEBVHIVKLLHLEKGTNRKSKPPAFKGMKVIIVLETPAPVCVETTYQDY 660
DB 601 CVMHVHTAIEBVHIVKLLHLEKGTNRKSKPPAFKGMKVIIVLETPAPVCVETTYQDY 660
QY 661 POLGRFTLRDQGTIIAGIKVIAE 685
DB 661 POLGRFTLRDQGTIIAGIKVIAE 685

RESULT 4
Q8TFR7 ID Q8TFR7 PRELIMINARY; PRT; 666 AA.
AC Q8TFR7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Prion protein.
GN Name=SUP35;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SCI14;
RX MEDLINE=22773310; PubMed=12890024;
RA Resende C.G., Outeiro T.F., Sands L., Lindquist S., Tuite M.F.;
RT "Prion protein gene polymorphisms in Saccharomyces cerevisiae.";
RL Mol. Microbiol. 49:1005-1017(2003).
DR EMBL; AY028647; AAK26178.1; -.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003747; F:translation release factor activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0006415; P:translational termination; IEA.
DR InterPro; IPR004160; EFTU_Cterm.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR009001; Elong_init_C.
DR InterPro; IPR000795; ProtSyn_GTPbind.
DR InterPro; IPR009000; Translat factor.
DR InterPro; IPR003285; Yeast ERF.
DR Pfam; PF00009; GTP_EFTU_1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR Pfam; PF03143; GTP_EFTU_D3; 1.
DR PRINTS; PR00315; ELONGATNFCT.
DR PRINTS; PR01343; YEASTERF.
DR PROSITE; PS00301; ERFATOR_GTP; UNKNOWN 1.
KW GTP-binding; Prion; Protein biosynthesis.
SQ SEQUENCE 666 AA; 74408 MW; 13EA65612A0705F8 CRC64;
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Query Match 96.1%; Score 3455.5; DB 2; Length 666;
Best Local Similarity 97.1%; Pred. No. 3.2e-168;
Matches 665; Conservative 0; Mismatches 1; Indels 19; Gaps 1;

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QY 1 MSDSNOGNQNTQYQYSONGNOQGNRYQGYQAYNAQAOPAGGYQNYQYSGYQGGY 60
DB 1 MSDSNOGNQNTQYQYSONGNOQGNRYQGYQAYNAQAOPAGGYQNYQYSGYQGGY 60
QY 61 QQYNPDAGYQQQYNPDAGYQQQYNPDAGYQQQYNPDAGYQQQYNPDAGYQQQYNPDAGY 120
DB 57 -----QGGYQQYNPDAGYQQQYNPDAGYQQQYNPDAGYQQQYNPDAGYQQQYNPDAGY 101
QY 121 SQGMSLNDFOKQKQAPKPKTKLVLSSSGIKLANATKKVGTGTPAESDKKEEKSAETK 180
DB 102 SQGMSLNDFOKQKQAPKPKTKLVLSSSGIKLANATKKVGTGTPAESDKKEEKSAETK 161
QY 181 EPTKEPTKVEPEVKKEKPVQTEETKEKSELKVEDLKIESTHTNTNANVTSDALIK 240
DB 162 EPTKEPTKVEPEVKKEKPVQTEETKEKSELKVEDLKIESTHTNTNANVTSDALIK 221
QY 241 EQEEVDDEVDNMFQGHVSLIFMGHVDAGKSTMGGNLLYLTGSDVKRTIEKYEREAK 300
DB 222 EQEEVDDEVDNMFQGHVSLIFMGHVDAGKSTMGGNLLYLTGSDVKRTIEKYEREAK 281
QY 301 DAGRGWYLSWVMDTNKEERNDGKTIIEVGKAYFETEKRRYTILDPAGHKMYVSEMIIGAS 360
DB 282 DAGRGWYLSWVMDTNKEERNDGKTIIEVGKAYFETEKRRYTILDPAGHKMYVSEMIIGAS 341
QY 361 QADVGVLLVLSARKGEYETGFERGGQTRHALLAKTQGVNKMVWVVKMDPTVWNSKERY 420
DB 342 QADVGVLLVLSARKGEYETGFERGGQTRHALLAKTQGVNKMVWVVKMDPTVWNSKERY 401
QY 421 DQCVSNVSNFLRAIGYNIKTDDVMPVSGYSGANLKDHDVDPKPCPWTGPTLLEYLDTMN 480
DB 402 DQCVSNVSNFLRAIGYNIKTDDVMPVSGYSGANLKDHDVDPKPCPWTGPTLLEYLDTMN 461
QY 481 HVDRHINAPFMLPIAAKMKDLGTTVEGKIESGHIKKGSTLLMPNKTAVEIQNIYNEN 540
DB 462 HVDRHINAPFMLPIAAKMKDLGTTVEGKIESGHIKKGSTLLMPNKTAVEIQNIYNEN 521
QY 541 EVDNMCGEQVKLRIGVEBEDISPGFVLTSPPKPIKSVTKFVAQIAIIVELKSIIAAGFS 600
DB 522 EVDNMCGEQVKLRIGVEBEDISPGFVLTSPPKPIKSVTKFVAQIAIIVELKSIIAAGFS 581
QY 601 CVMHVHTAIEBVHIVKLLHLEKGTNRKSKPPAFKGMKVIIVLETPAPVCVETTYQDY 660
DB 582 CVMHVHTAIEBVHIVKLLHLEKGTNRKSKPPAFKGMKVIIVLETPAPVCVETTYQDY 641
QY 661 POLGRFTLRDQGTIIAGIKVIAE 685
DB 642 POLGRFTLRDQGTIIAGIKVIAE 666

RESULT 5
Q8TFR8 ID Q8TFR8 PRELIMINARY; PRT; 666 AA.
AC Q8TFR8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Prion protein.
GN Name=SUP35;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SCI3;
RX MEDLINE=22773310; PubMed=12890024;
RA Resende C.G., Outeiro T.F., Sands L., Lindquist S., Tuite M.F.;
RT "Prion protein gene polymorphisms in Saccharomyces cerevisiae.";
RL Mol. Microbiol. 49:1005-1017(2003).
DR EMBL; AY028646; AAK26177.1; -.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003747; F:translation release factor activity; IEA.
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QY 273 KSTWGGNLLYLTSVDRKRTIEKYBREAADAGROGWYLSWMDTNKEBRNDGKTIIEVGKAY 332
DB 276 KSTWGGNLLYLTSVDRKRTIEKYBREAADAGROGWYLSWMDTNKEBRNDGKTIIEVGKAY 335
QY 333 FETEKRRYITILDAPGHKMYSEMIGGASQADVGVLVTSARKGEYETGFERGGQTRHALL 392
DB 336 FETEKRRYITILDAPGHKMYSEMIGGASQADVGVLVTSARKGEYETGFERGGQTRHALL 395
QY 393 AKTOGVNKMVVVNMDDPTVNSKERYDQCVSNVSNFLRAIGHNITKTDVVFMPVSYSG 452
DB 396 AKTOGVNKMVVVNMDDPTVNSQERYDQCVSNLSNLYKAIGNVQDVVFMPVSYSG 455
QY 453 ANLKDHVDPKCEPNYTGPTLLELYDTNHNVDHRHNAPFPLPIAAKMDLGTIVGKTESG 512
DB 456 AGLKERVKCEPNYDGPALLEYLDEMKVDRHVNAPFPLPIASKMDLGTIVGKTESG 515
QY 513 HIKKGQSTLLMPNKTAVEIQNIYNETENEVDMAKMGQVQLRIKGVBEEDISPGFVLTS 572
DB 516 HIKKGQSTLLMPNKIPVEIQNIYNETENEVDMAKMGQVQLRIKGVBEEDISAGFVLTS 575
QY 573 KNPITSVTKFVAQIAIVELKSIITAAAGSCVMHVHTAIEEVHIVKLLHLEKGTNRKSKKP 632
DB 576 KNPITKNVTRFVAQIAIVELKSIIMSAAGSCVMHVHTAIEEVHITRLHLKLRGTNRKSKKP 635
QY 633 PAFAKKGMKVIATLEAPVCVETQYDYPQLGRFTLRDQGTIIAGKIVKIAE 685
DB 636 PAFAKKGMKIIATLEAPVCVETQYDYPQLGRFTLRDQGTIIAGKIVKILE 688

RESULT 7
Q9HGI4 PRELIMINARY; PRT; 662 AA.
ID Q9HGI4
AC Q9HGI4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polypeptide release factor 3.
GN Name=sup35;
OS Zygosaccharomyces rouxii (Candida mogii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.
OX NCBI_TaxID=4956;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21324710; PubMed=11430816; DOI=10.1016/S1097-2765(01)00259-3;
RA Nakayashiki T., Ebihara K., Bannai H., Nakamura Y.;
RT "Yeast [PSI+] 'prions' that are crosstransmissible and susceptible
RL Mol. Cell 7:1121-1130(2001).
DR EMBL; AB039753; BAB12684.2; -.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003747; P:translation release factor activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0006415; P:translational termination; IEA.
DR InterPro; IPR004160; EFTU_Cterm.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR009001; Elong_init_C.
DR InterPro; IPR000795; ProtSyn_GTPbind.
DR InterPro; IPR009000; Translat_factor.
DR InterPro; IPR003285; Yeast_ERF.
DR Pfam; PF00009; GTP_EFTU_1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR Pfam; PF03143; GTP_EFTU_D3; 1.
DR PRINTS; PR00315; ELONGATNFCT.
DR PRINTS; PR01343; YEASTERF.
DR PROSITE; PS00301; EFACOR_GTP; UNKNOWN_1.
KW GTP-binding; Protein biosynthesis.
SQ SEQUENCE 662 AA; 73780 MW; 2841046199FB1E04 CRC64;

Query Match 70.9%; Score 2549.5; DB 2; Length 662;
Best Local Similarity 74.0%; Pred. No. 5.2e-122;
Matches 512; Conservative 53; Mismatches 90; Indels 37; Gaps 15;
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QY 1 MSDSNQNNQNTQOYQYSONGNOQOQNNRYQGY-QAYNAOQAPAGGYQNTQYSGYQOQG 59
DB 1 MSDPNQ-NGQ-----QGGQOAGNNTQOYFQKLTQQAQ-AGGGYQPYGGYGY--GG 49
QY 60 YOYNPDAGYQOQYFNPQGGYQ-QYNPQGGYQOQFNPQGGRGNYKNFNNNNLLQYQAGFQ 118
DB 50 YGYQPYGGYQOQFY--QDGOQAQOQAYNGYPYQ--AQGAPGGFN--NYYNQFQP-----Q 98
QY 119 PQSQGSLNDPQOQ---KQAAAPKPKTKTLVSSSGIKLANATKVKGTKPAESDKKEEK 175
DB 99 QSQGQMTLDDPHKQKTSQSPAPFKQKSLKLVSSSGIKLANATK---KPKKEDEKKEEP 154
QY 176 SATK--EPTKPTKVEEPVKKEKPVQTEKTEEKSLEPKVEDLKISETHTNNTNANVT 233
DB 155 KKEEKAAPKEQSKKEEP-KREGTPPAAAKDEKEDLEPKELKIKE---EQAAANAS 210
QY 234 SADALIKEQEEVEEDVNDMFGGDHVSILFMGHVDAGKSTMGGNLLYLTGSDVKRTIE 293
DB 211 GADSLIKEQEEVEEDGVNDMFGGDHMSIIFMGHVDAGKSTMGGNILYMTGSDVKRTVE 270
QY 294 KYREAKDAGROGWYLSWMDTNKEBRNDGKTIIEVGKAYFETEKRRYITILDAPGHKMY 353
DB 271 KYREAKDAGROGWYLSWMDTNKEBRNDGKTIIEVGKAYFETEKRRYITILDAPGHKMY 330
QY 354 EMIGGASQADVGVLVTSARKGEYETGFERGGQTRHALLAKTOGVNKMVVVNMDDPTV 413
DB 331 EMIGGASQADVGVLVTSARKGEYETGFERGGQTRHALLAKTOGVNKLIVTNKMDPTV 390
QY 414 NWSKERYDQCVSNVSNFLRAIGNIKTDVVFMPVSYSGANLKHVDPKCEPNYTGPTLL 473
DB 391 NWSKERYDQCVKLSNPLKAIGNVKEEVVMPVSYSGAGLGTTRVDPKCEPNYDGPALL 450
QY 474 EYLDTNHVDHRHNAPFPLPIAAKMDLGTIVGKTESGHIKKGQSTLLMPNKTAVEIQ 533
DB 451 EYMDNMSHVDRKNVAPFPLPIAAKMDMGTVFSGKIESGHIRKGHSTLLMPNKIPVEIQ 510
QY 534 IYNETENEVDMAKMGQVQLRIKGVBEEDISPGFVLTSKPNPKSVTKFVAQIAIVELKS 593
DB 511 IYNETENEVDMAKMGQVQLRIKGVBEEDISPGFVLTSKPNPKSVTRFVAQIAIVELKS 570
QY 594 IIAAGSCVMHVHTAIEEVHIVKLLHLEKGTNRKSKPPAFKMGKVIATLEAPVC 653
DB 571 ILSGFSFCVMHVHTAIEEVHITKLLHLKLRGTNRKSKPPAFKMGKVIATLEAPVC 630
QY 654 VETQYDYPQLGRFTLRDQGTIIAGKIVKIAE 685
DB 631 VETQYDYPQLGRFTLRDQGTIIAGKIVKIIIE 662

RESULT 8
Q6CQF8 PRELIMINARY; PRT; 700 AA.
ID Q6CQF8
AC Q6CQF8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similarity.
GN ORFNames=KLLA0D17424g;
OS Kluyveromyces lactis NRRL Y-1140.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=284590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
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QY 156 NATKVGCTKPAESDKKEEKSAAETKEPTKVEEPVKKEKFPVQTEETEEKSELSPKV 215
DB 171 GAKKVPAPK-----TEKIDSEKATK-----TTDDNEEAQSELPKI 206
QY 216 EDLKISE-----STHNTNANVTSA-----DALIKEQEEVEEDDEVN 252
DB 207 DLLKISEAEKPKTKENTPSSADDTSSSEKTSKADTSTGGANSVDALLIKEQEEVEDEVN 266
QY 253 DMFGGKHVSLIFMGHVDAGKSTWGNLLYLITGSDVDRTEKTEKREKADAGROGWYLSWV 312
DB 267 DMFGGKHVSLIFMGHVDAGKSTWGNLLYLITGSDVDRTEKTEKREKADAGROGWYLSWV 326
QY 313 MDTNKEERNDGKTEVGKAYFETEKRRYTTILDAPGHKMYSEMITGGASQADVGVLVLSAR 372
DB 327 MDTNKEERNDGKTEVGKAYFETEKRRYTTILDAPGHKMYSEMITGGASQADIGILVLSAR 386
QY 373 KGEYETGFERGGQTRHALLAKTOGVNKMVVVNMKDDPTVNSKERYDQCVSNVSNFLR 432
DB 387 KGEYETGFERGGQTRHALLAKTOGVNKMIVVINKMDDPTVNDKERYDHCVGNLTFLK 446
QY 433 AIGNVIKTDVFMVPSVSGANLKHVDPKCEPWYTGPTLLEYLDTNHHVDRHINAPFML 492
DB 447 AVGNVVKEDVIFMVPVSGYTGAGLKERVDPKDCPWYTGPTLLEYLDTNHHVDRHINAPFML 506
QY 493 PIARKMKDLGTIVGKIESGHIKKGQSTLMPNKTAVEIQNIYNETENEVDMAKMGQVX 552
DB 507 PIASKMDMGVVBEGKIESGHIRGNQTLMPNRTSVEIITINETSEVDMAKMGQVX 566
QY 553 LRIKGVBEEDISPQFVLTSPPNPIKSVTKFVAQIAVELKSIIAAGFSCVMHVTAEV 612
DB 567 LRIKGVBEEDISPQFVLTSPPNPNVTRFVAQIAVELKSINSAGSCVMHVTAEV 626
QY 613 HIVKLLHLEKGTNRKSKPPAPAKGKMKVIAVLEAPVCVETIYQYPOLGRFTLRDQ 672
DB 627 TVTRLHLKLGKSNRKSPPAPAKGKMKVIAVLEAPVCVETIYQYPOLGRFTLRDQ 686
QY 673 TTTAIGKIVKIAE 685
DB 687 TTTAIGKIVKILE 699

RESULT 10
Q750T4 PRELIMINARY; PRT; 691 AA.
AC Q750T4
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AGL145wp.
GN ORFNames=AGL145W;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10895;
RA Lerch A., Brachat S., Voegel S.E., Gaffney T., Philippsen P.,
RA Dietrich F.S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016820; AAS54346.1; -.
DR AGD; AGL145W; -.
DR GO; GO:0005255; F:GTP binding; IEA.
DR GO; GO:0003747; P:translation release factor activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0006415; P:translational termination; IEA.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR009001; Elong_init_C.
DR InterPro; IPR00795; ProtSyn_GTPbind.
DR InterPro; IPR009000; Translat factor.
DR InterPro; IPR003285; Yeast ERF.
DR Pfam; PF00009; GTP_EFTU; 1.

QY 156 NATKVGCTKPAESDKKEEKSAAETKEPTKVEEPVKKEKFPVQTEETEEKSELSPKV 215
DB 171 GAKKVPAPK-----TEKIDSEKATK-----TTDDNEEAQSELPKI 206
QY 216 EDLKISE-----STHNTNANVTSA-----DALIKEQEEVEEDDEVN 252
DB 207 DLLKISEAEKPKTKENTPSSADDTSSSEKTSKADTSTGGANSVDALLIKEQEEVEDEVN 266
QY 253 DMFGGKHVSLIFMGHVDAGKSTWGNLLYLITGSDVDRTEKTEKREKADAGROGWYLSWV 312
DB 267 DMFGGKHVSLIFMGHVDAGKSTWGNLLYLITGSDVDRTEKTEKREKADAGROGWYLSWV 326
QY 313 MDTNKEERNDGKTEVGKAYFETEKRRYTTILDAPGHKMYSEMITGGASQADVGVLVLSAR 372
DB 327 MDTNKEERNDGKTEVGKAYFETEKRRYTTILDAPGHKMYSEMITGGASQADIGILVLSAR 386
QY 373 KGEYETGFERGGQTRHALLAKTOGVNKMVVVNMKDDPTVNSKERYDQCVSNVSNFLR 432
DB 387 KGEYETGFERGGQTRHALLAKTOGVNKMIVVINKMDDPTVNDKERYDHCVGNLTFLK 446
QY 433 AIGNVIKTDVFMVPSVSGANLKHVDPKCEPWYTGPTLLEYLDTNHHVDRHINAPFML 492
DB 447 AVGNVVKEDVIFMVPVSGYTGAGLKERVDPKDCPWYTGPTLLEYLDTNHHVDRHINAPFML 506
QY 493 PIARKMKDLGTIVGKIESGHIKKGQSTLMPNKTAVEIQNIYNETENEVDMAKMGQVX 552
DB 507 PIASKMDMGVVBEGKIESGHIRGNQTLMPNRTSVEIITINETSEVDMAKMGQVX 566
QY 553 LRIKGVBEEDISPQFVLTSPPNPIKSVTKFVAQIAVELKSIIAAGFSCVMHVTAEV 612
DB 567 LRIKGVBEEDISPQFVLTSPPNPNVTRFVAQIAVELKSINSAGSCVMHVTAEV 626
QY 613 HIVKLLHLEKGTNRKSKPPAPAKGKMKVIAVLEAPVCVETIYQYPOLGRFTLRDQ 672
DB 627 TVTRLHLKLGKSNRKSPPAPAKGKMKVIAVLEAPVCVETIYQYPOLGRFTLRDQ 686
QY 673 TTTAIGKIVKIAE 685
DB 687 TTTAIGKIVKILE 699

RESULT 10
Q750T4 PRELIMINARY; PRT; 691 AA.
AC Q750T4
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AGL145wp.
GN ORFNames=AGL145W;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10895;
RA Lerch A., Brachat S., Voegel S.E., Gaffney T., Philippsen P.,
RA Dietrich F.S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016820; AAS54346.1; -.
DR AGD; AGL145W; -.
DR GO; GO:0005255; F:GTP binding; IEA.
DR GO; GO:0003747; P:translation release factor activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0006415; P:translational termination; IEA.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR009001; Elong_init_C.
DR InterPro; IPR00795; ProtSyn_GTPbind.
DR InterPro; IPR009000; Translat factor.
DR InterPro; IPR003285; Yeast ERF.
DR Pfam; PF00009; GTP_EFTU; 1.
```

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DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR PRINTS; PR00315; ELONGATNFC.
DR PRINTS; PR01343; YEASTERE.
DR PROSITE; PS00301; EFACOR_GTP; UNKNOWN_1.
KW GTP-binding; Protein biosynthesis.
SQ SEQUENCE 691 AA; 76193 MW; 8B38099C60EB9509 CRC64;

Query Match 68.6%; Score 2464; DB 2; Length 691;
Best Local Similarity 71.1%; Pred. No. 1.3e-117; Indels 58; Gaps 17;
Matches 500; Conservative 52; Mismatches 93;

QY 5 NOGNNOQNYOQYSONGNOQGNRYQY---QAYNAQAQAGGY--YQNYQ----GYSGY 55
DB 25 NQGGQGNFQYQNPSPNFQ---NYQYVPGGYQAYGQAGGYQYQAYNQOAGGYQY 80
QY 56 QQGGYQOYNP-DAGYQOQYNPQGYQOYNPQGYQ--QGFN--POGGRNYKPNYNNL 110
DB 81 Q--GYOQYNPAQGYQ-----GYOQYNAQGYQSYKQYNSQPGNKRKNQSYGYG-- 128
QY 111 QGYQAGFQPOSQGSMLNDFOK--QKQAAAPKPKTLKLVSSSGIKLANATKVKTKPAES 168
DB 129 QG-----QSATAPVTLLNFEKGTVPNATAPKPKTLKLASSSGIKLVCAKKPVA-- 177
QY 169 DKKEEKSAAETKEPTK--VEEPVKKEKPVQTEETEEKSELPKVEDLKISES--- 223
DB 178 -KKEE---AKAESPTEEKPSAEGAPKSDATASEDKA-----VPSIEKLSISEADTA 228
QY 224 -THTNNANVTSDALIKEQEEVEEDDEVNDFMGKDHVSLIPMGHVDAGKSTWGNLLY 282
DB 229 KQDTAAGATSSDALIKEQEEVEEDDEVNDFMGKDHVSLIPMGHVDAGKSTWGNLLY 288
QY 283 LTGSVDKRTTEKTEREAKDAGRWYLSWMDTNKEERNDGKTEVGKAYFETEKRYTI 342
DB 289 LTGSVDKRTTEKTEREAKDAGRWYLSWMDTNKEERNDGKTEVGKAYFETEKRYTI 348
QY 343 LDAPGHKMYSEMITGGASQADVGVLVISARKGYETGFERGGQTRHALLAKTOGVNKMV 402
DB 349 LDAPGHKMYSEMITGGASQADVGVLVISARKGYETGFERGGQTRHALLAKTOGVNKMV 408
QY 403 VVYNKMDPTVNSKERYDQCVSNVSNFLRAIGNIKTDVFMVPSVSGANLKHVDPK 462
DB 409 VVYNKMDPTVNDKARYDQCIKNVSNFLOAIGNVKEDVYMPVSGFTGAGLKDRVDKK 468
QY 463 ECPWYGTPTLLEYLDTNHHVDRHINAPFMLPIAAKMKDLGTIVGKTESGHIKKGQSTLL 522
DB 469 DCPWYDGPLLLEYLDTNHHVDRFINAPFMLPIASKMDMGTVVEGKIESGHIKKGQSTLL 528
QY 523 MPNKTAVEIQNIYNETENEVDMAKMGQVQLRKINGVEEEDISPQFVLTSPPNPIKSVTKF 582
DB 529 MPNKIPVEILAIQNETEQEVDMAVCGQVRLRLKGVVEEDISAGFVLTSPPNPKVNTKF 588
QY 583 VAQIAVELKSIIAAGFSCVMHVTAEVHIVKLLHLEKGTNRKSKPPAPAKGKMKV 642
DB 589 VDQIAVELKSINSAGFSCVMHVTAEVSIITRLHLKLEKGTNRKSKPPAPAKGKMKI 648
QY 643 IAVLETEAPVCVETIYQYPOLGRFTLRDQGTITTAIGKIVKIAE 685
DB 649 IAVLETEAPVCVETIYQYPHLGRFTLRDQGTITTAIGKIVKILE 691

RESULT 11
Q9HGI7 PRELIMINARY; PRT; 712 AA.
AC Q9HGI7
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polypeptide release factor 3.
GN Name=sup35;
OS Candida maltosa (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5479;
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QY 55 YQQ-QGYQQYNP-DAGYQQQYVPOGGYQQ-YNPQGGYQQQFNPOGGRGNYKNFNNNNLQ 111
DB 54 QQQYGGYNQYQGGYQQYNNRGGYQQGYNRGGYQQYNN---NRGGYQQGNNQQYQ 110
QY 112 GYQA-GFQP-----SQSGMSLNDFOKQ--QKQAA---PKPKTKTLKLVSSSGIKLANATK 159
DB 111 GYQYNSQPQQQQQQSQSGMSLADFQKQKTEQQQASLNKPAVKTKTLKLAGSSGIKLANATK 170
QY 160 KVGTT--KP-----AESDKBEKSAETKEP-----TKEPTKVEEPVK 194
DB 171 KVDTTSPQSKESPAPAPAAASASASAPQEBKEKEKEAAAAAPAAETTKETKTSAPAEK 230
QY 195 KEKPVOTEETKESKSELKVEDLKISESTHTNNVTSADALIKEQEEVEVDVVNDM 254
DB 231 KEATP--TPAANKNESTIPAAAANK--ESTPVSNSASVATADALKEQDEIDEVEVNDM 286
QY 255 FGGKDHVSLIFMGHVDAGKSTMGGNLLYLTGSDVDKRTIEKYEREAKDAGRGWYLSWMD 314
DB 287 FGGKDHVSLIFMGHVDAGKSTMGGNLLYLTGSDVDKRTVEKYEREAKDAGRGWYLSWMD 346
QY 315 TNKEERNDGKTIEVGKAYFETEKRRYTLDPAGHKMTVSEMIIGGASQADVGLVISARKG 374
DB 347 TNKEERNDGKTIEVGKAYFETDKERYTLDPAGHKMTVSEMIIGGASQADVGLVISARKG 406
QY 375 EYETGPERGGOTREHALLAKTQGVNKMVVVNKMDPTVNWSKERYDQCVSNYNELRAI 434
DB 407 EYETGFEGKGGOTREHALLAKTQGVNKKIIVVNKMDSTVGMSKERYQECITKLGAFLKI 466
QY 435 GYNLKTDFVMPVPSVSGYGANLKHVDPKCEPWYTGPTLLLEYLDTFMNVHVRHINAPFMPLI 494
DB 467 GY-AKDDIIYNPVSQYTGAGLKDQVDPKDCPWYDGPSSLEVLNDMNTWNRKINGPFMPV 525
QY 495 AAKMKDLGTIVGKIESGHIKKGOSTLLMPNKTAVEIQNIYNETENEVDAMCQEQVKLR 554
DB 526 SGKMKDLGTIVGKIESGHHVKNLIMPNKPTPIEVLTFNETEPOBCDTAFSGEQVRLK 585
QY 555 IKGVEEEDISPGVLTSPKPKIKSVTKFVAQIAIVELKSLIAAGFSCVMHVHTAIEVHI 614
DB 586 IKGIEEDLQPGYVLTSPKPNKVTTRPEAQIAIVELKSLILNSGFSCVMHLHTAIEVKF 645
QY 615 VKLHLKEKGTNRKSKPPAPFAKGMKVIAVLETEAPVCVETYQDYPQLGRFTLRDQGT 674
DB 646 IELGHLEKGTNRKSKPPAPFAKGMKIIALLEVGELVCAETKYDYPQLGRFTLRDQGT 705
QY 675 IAIKGIKVI 683
DB 706 IAIKGIKTL 714

RESULT 13

Q6Q7I3 PRELIMINARY; PRT; 435 AA.
ID Q6Q7I3;
AC Q6Q7I3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Translation termination factor SUP35 (Fragment).
GN Name=SUP35;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M22, S288C, and M8;
RX PubMed=15059259;
RA Fay J.C., McCullough H.L., Sniegowski P.D., Eisen M.B.;
RT "Population genetic variation in gene expression is associated with
phenotypic variation in Saccharomyces cerevisiae.";
RL Genome Biol. 5:R26-R26(2004).
DR EMBL; AY553987; AAS64328.1; -.
DR EMBL; AY553990; AAS64331.1; -.
DR EMBL; AY553985; AAS64326.1; -.
DR GO; 0005525; F:GTP binding; IEA.
DR GO; 0003747; F:translation release factor activity; IEA.
DR GO; 0006412; P:protein biosynthesis; IEA.
DR GO; 0006415; P:translational termination; IEA.
DR InterPro; IPR000795; ProtSyn GTPbind.
DR InterPro; IPR003285; Yeast ERF.
DR PRINTS; PR00315; ELONGATNFCT.
DR PRINTS; PR01343; YEASTERF.
DR PROSITE; PS00301; EFATOR_GTP; UNKNOWN_1.
KW GTP-binding; Protein biosynthesis.
FT NON TER 1 1
FT NON TER 435 435
SQ SEQUENCE 435 AA; 48968 MW; ED0E85699BB28442 CRC64;

Query Match 64.1%; Score 2303; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.1e-109;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NNQNTQOQYSONGNOQGNRRYQGYQAYNAQAOPAGGYQNYQYSGYQGGYQQYNPDA 67
DB 1 NNQNTQOQYSONGNOQGNRRYQGYQAYNAQAOPAGGYQNYQYSGYQGGYQQYNPDA 60
QY 68 GYQQYNPQGGYQOYNPQGGYQQQFNPQGGRGNYKNFNNNNLQGYQAGFQPSQGSMLN 127
DB 61 GYQQYNPQGGYQOYNPQGGYQQQFNPQGGRGNYKNFNNNNLQGYQAGFQPSQGSMLN 120
QY 128 DFQKQQAAPKPKTKTLKLVSSSGIKLANATKKVGTKPAESDKKEEKSAETKEPTKEPT 187
DB 121 DFQKQQAAPKPKTKTLKLVSSSGIKLANATKKVGTKPAESDKKEEKSAETKEPTKEPT 180
QY 188 KVEEPVKKEKPVQTEKTEKSELKVEDLKISESTHTNNVTSADALIKEQEEVEVD 247
DB 181 KVEEPVKKEKPVQTEKTEKSELKVEDLKISESTHTNNVTSADALIKEQEEVEVD 240
QY 248 DEVVNDMFGGKDHVSLIFMGHVDAGKSTMGGNLLYLTGSDVDKRTIEKYEREAKDAGRGW 307
DB 241 DEVVNDMFGGKDHVSLIFMGHVDAGKSTMGGNLLYLTGSDVDKRTIEKYEREAKDAGRGW 300
QY 308 YLSWMDTNKEERNDGKTIEVGKAYFETEKRRYTLDPAGHKMTVSEMIIGGASQADVGL 367
DB 301 YLSWMDTNKEERNDGKTIEVGKAYFETEKRRYTLDPAGHKMTVSEMIIGGASQADVGL 360
QY 368 VISARKGEYETGPERGGOTREHALLAKTQGVNKMVVVNKMDPTVNWSKERYDQCVSNV 427
DB 361 VISARKGEYETGPERGGOTREHALLAKTQGVNKMVVVNKMDPTVNWSKERYDQCVSNV 420
QY 428 SNFLRAIGYNIKTDV 442
DB 421 SNFLRAIGYNIKTDV 435

RESULT 14

Q6Q7I6 PRELIMINARY; PRT; 435 AA.
ID Q6Q7I6;
AC Q6Q7I6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Translation termination factor SUP35 (Fragment).
GN Name=SUP35;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M5;
RX PubMed=15059259;
RA Fay J.C., McCullough H.L., Sniegowski P.D., Eisen M.B.;
RT "Population genetic variation in gene expression is associated with
phenotypic variation in Saccharomyces cerevisiae.";
RL Genome Biol. 5:R26-R26(2004).

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2005, 18:05:05 ; Search time 191.103 Seconds

(without alignments)
1386.327 Million cell updates/sec

Title: US-09-591-632-2

Perfect score: 3594

Sequence: 1 MSDSNQGNQNYQQYQSQNG.....FTLRDQGTIIAGIKIVKIAE 685

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: _geneseqp1980s:.*
2: _geneseqp1990s:.*
3: _geneseqp2000s:.*
4: _geneseqp2001s:.*
5: _geneseqp2002s:.*
6: _geneseqp2003as:.*
7: _geneseqp2003bs:.*
8: _geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3594	100.0	685	4 AAB30792	Aab30792 Amino aci
2	3594	100.0	685	6 ABR53107	Abr53107 Protein s
3	3594	100.0	685	7 ADK63022	Adk63022 Disease t
4	2347.5	65.3	721	5 ABP73437	Abp73437 Candida a
5	2345.5	65.3	715	4 AAB30820	Aab30820 Amino aci
6	2177	60.6	741	4 AAB30819	Aab30819 Amino aci
7	1679.5	46.7	690	8 ADS44300	AdS44300 Bacterial
8	1658	46.1	720	7 ADB70240	AdB70240 C. neofo
9	1517.5	42.3	716	6 ABJ26050	AbJ26050 Aspergill
10	1519.5	43.3	712	6 ABJ25450	AbJ25450 Aspergill
11	1364.5	38.0	634	7 ADM04489	Adm04489 Human pro
12	1354.5	37.7	499	7 ADC35080	Adc35080 Human bre
13	1354.5	37.7	499	8 ADN03793	Adn03793 Antipsori
14	1354.5	37.7	499	8 ADP54304	Adp54304 Human PRO
15	1354.5	37.7	499	8 ADP24765	Adp24765 PRO poly
16	1354.5	37.7	499	8 ADR99225	Adr99225 G1 to S p
17	1346.5	37.5	628	8 AAN99777	Adn99777 Novel hum
18	1345.5	37.4	628	4 AAB92825	Aab92825 Human pro
19	1329	37.0	271	4 AAB30800	Aab30800 A modifie
20	1316.5	36.6	619	4 ABB62309	Abb62309 Drosophi
21	1307.5	36.4	499	2 AAW37508	Aaw37508 Human GSP
22	1307.5	36.4	499	6 ABR56523	Abr56523 Human GSP
23	1307.5	36.4	499	8 AQO76519	Aqo76519 Amino aci
24	1260	35.1	504	4 AAB94470	Aab94470 Human pro
25	1097	30.5	215	4 AAB30799	Aab30799 A modifie

26	922.5	25.7	684	4 AAB68535	Aab68535 Human GNP
27	920.5	25.6	684	4 AAB95757	Aab95757 Human pro
28	825	23.0	661	4 ABB58653	Abb58653 Drosophi
29	824	22.9	449	7 ADD90630	Add90630 Porphyra
30	823.5	22.9	408	5 ABB90306	Abb90306 Human pol
31	823	22.9	460	8 ADS44204	AdS44204 Bacterial
32	822	22.9	460	8 ADN19715	Adn19715 Bacterial
33	817.5	22.7	408	2 AAY27924	Aay27924 Human sec
34	817.5	22.7	408	6 ABO14428	AbO14428 Novel hum
35	817.5	22.7	408	8 ADG78836	Adg78836 Human sec
36	817.5	22.7	408	8 ADN61126	Adn61126 Human sec
37	808	22.5	449	7 ADC81653	Adc81653 Leishmani
38	801.5	22.3	447	2 AAR31594	Aar31594 61-1 clon
39	801.5	22.3	462	2 AAW11237	Aaw11237 Elongatio
40	799.5	22.2	460	2 AAW36114	Aaw36114 Yeast elo
41	798.5	22.2	448	2 AAR05565	Aar05565 Plant elo
42	798.5	22.2	448	2 AAR31595	Aar31595 LeEF-1 cl
43	798.5	22.2	449	3 AAG45359	Aag45359 Arabidops
44	798.5	22.2	449	3 AAG47144	Aag47144 Arabidops
45	798.5	22.2	449	3 AAG35730	Aag35730 Arabidops

ALIGNMENTS

RESULT 1
AAB30792
ID AAB30792 standard; protein; 685 AA.
XX
AC AAB30792;
XX
DT 02-APR-2001 (first entry)
XX
DE Amino acid sequence of a yeast Sup35 protein.
XX
KW Sup35; phenotype: SCHAG; self-coalesce; higher-order aggregate;
KW amyloidogenic domain; aggregation; fibril; phenotypic alteration;
KW gene therapy; disease resistance; plant pigmentation; prion disease.
XX
OS Saccharomyces cerevisiae.
XX
FN WO200075324-A2.
XX
PD 14-DEC-2000.
XX
PF 09-JUN-2000; 2000WO-US015876.
XX
PR 09-JUN-1999; 99US-0138833P.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Lindquist S, Li L, Ma J, Liu J, Sondheimer N, Scheibel T;
XX
WPI; 2001-061723/07.
XX
N-PSDB; AAC86679.
XX
New nucleic acid encoding chimeric proteins with self-assembly properties, useful e.g. for diagnosis and treatment of prion diseases, also related aggregates, fibrils and polymers.
XX
Claim 11; Page 125-127; 188pp; English.
XX
The present sequence represents a yeast Sup35 protein. The protein possesses the prion-like capacity to undergo a self-perpetuating conformational alteration that changes the functional state of Sup35 in a manner that creates a heritable change in phenotype. It is used to construct chimeric polypeptides of the invention, which comprise at least one SCHAG (self-coalesce into higher-order aggregates) amino acid sequence fused in frame with a polypeptide of interest (which is other than a marker protein, a glutathione-S-transferase or a staphylococcal nuclear protein). The specification also describes chimeric polypeptides that comprises an amyloidogenic domain that causes aggregation into fibrils. The chimeric polypeptides are used to prepare polymers with

Qy 421 DQCVSNVSNFLRAIGYNIKTVDVMPVSGYSGANLKHVDPKPCPWTGPTLLLEYLDTMN 480
Db 421 DQCVSNVSNFLRAIGYNIKTVDVMPVSGYSGANLKHVDPKPCPWTGPTLLLEYLDTMN 480
Qy 481 HVDRHINAPFMLPIAAKMKDLGTTVEGKIESGHKKKGSTLLMPNKTAVEIQNIYNENET 540
Db 481 HVDRHINAPFMLPIAAKMKDLGTTVEGKIESGHKKKGSTLLMPNKTAVEIQNIYNENET 540
Qy 541 EVDNMGCEQVKLRKIGVEEEDISPGFVLTSPPKPIKSVTFKVAQIAIVELKSIAGFS 600
Db 541 EVDNMGCEQVKLRKIGVEEEDISPGFVLTSPPKPIKSVTFKVAQIAIVELKSIAGFS 600
Qy 601 CVMHVHTAIEBVHIVKLLHLEKGTNRKSKPPAPAKGMKVIAVLETEAPVCVETYQDY 660
Db 601 CVMHVHTAIEBVHIVKLLHLEKGTNRKSKPPAPAKGMKVIAVLETEAPVCVETYQDY 660
Qy 661 POLGRFTLRDQGTIIAIGKIVKIAE 685
Db 661 POLGRFTLRDQGTIIAIGKIVKIAE 685

RESULT 3

ID ADK63022 standard; protein; 685 AA.
XX
AC ADK63022;

DT 06-MAY-2004 (first entry)

XX Disease treating protein complex-derived protein #637.

XX protein complex; drug target; diagnosis.

XX Unidentified.

XX EPI338608-A2.

XX 27-AUG-2003.

XX 20-DEC-2002; 2002EP-00102902.

XX 20-DEC-2001; 2001EP-00130253.

XX (CELL-) CELLZOME AG.

PI Bauer A, Gavin A, Supertli-Furga G, Kuester B, Schultz J;
PI Marzioch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;
PI Michon A, Leutwein C, Rick J;

XX WPI; 2003-638460/61.

DR N-PSDB; ADK63023.

XX New proteins and protein complexes from eukaryotes, useful as targets in
PT drug screening, or in diagnosing or screening for the presence of a
PT disease or disorder, or a predisposition for developing a disease or
PT disorder in a subject.

PS Disclosure; SEQ ID NO 1273; 13pp; English.

XX The invention relates to novel protein complexes comprising a first and a
CC second protein, or its derivative, fragment, homologue or variant. The
CC proteins are selected from given protein complexes, which are not defined
CC in the specification. The variants are encoded by nucleic acids that
CC hybridize to the nucleic acids encoding the proteins under low stringency
CC conditions. The protein complexes are useful as targets for an active
CC agent of a pharmaceutical. These protein complexes are particularly
CC useful as drugs targets for the treatment or preventing of a disease or
CC disorder. The complexes and methods above are useful in diagnosing or
CC screening for the presence of a disease or disorder or a predisposition
CC for developing a disease or disorder in a subject. These are also useful
CC in screening for a drug for treatment or prevention of a disease or
CC disorder. The molecule that modulates the amount, activity or protein
CC components of the complex is useful for the manufacture of a medicament

CC for the treatment or prevention of a disease or disorder. This sequence
CC corresponds to a protein of the invention. (Note: the sequence data for
CC this patent did not form part of the printed specification but was
CC obtained from the EPO in electronic format).

XX Sequence 685 AA;

Query Match 100.0%; Score 3594; DB 7; Length 685;
Best Local Similarity 100.0%; Pred. No. 2.9e-241; Gaps 0;
Matches 685; Conservative 0; Mismatches 0; Indels 0;

Qy 1 MSDSNQGNQOQYQOYSGNGNQOQGNRYQGYAYNAQAQAGGYQYQYSGYQOQGY 60
Db 1 MSDSNQGNQOQYQOYSGNGNQOQGNRYQGYAYNAQAQAGGYQYQYSGYQOQGY 60
Qy 61 QOYNPDAGYQOQYNPQGGYQOYNPQGGYQOYNPQGGYQOYNPQGGYQOYNPQGGY 120
Db 61 QOYNPDAGYQOQYNPQGGYQOYNPQGGYQOYNPQGGYQOYNPQGGYQOYNPQGGY 120
Qy 121 SQGSLNDFQKQKQAAPKPKTKLKVSSSGIKLANATKKVGTKPAESDKKEEKSATK 180
Db 121 SQGSLNDFQKQKQAAPKPKTKLKVSSSGIKLANATKKVGTKPAESDKKEEKSATK 180
Qy 181 EPTKEPTKVEBPVKKEKPVOTEKTEKSELKPKVEDLKISESTHNTNNAVTSADALIK 240
Db 181 EPTKEPTKVEBPVKKEKPVOTEKTEKSELKPKVEDLKISESTHNTNNAVTSADALIK 240
Qy 241 EQEEVDDEVVNDMFGGKHVSLIFMGHVDVADGKSTMGGNLLYLTGSDVKRTIEKYEBAK 300
Db 241 EQEEVDDEVVNDMFGGKHVSLIFMGHVDVADGKSTMGGNLLYLTGSDVKRTIEKYEBAK 300
Qy 301 DAGRQGYLWVMDTNKEERNDGKTIIEVGKAYFETEKRRYTLIDAPGHKMYVSEMGAS 360
Db 301 DAGRQGYLWVMDTNKEERNDGKTIIEVGKAYFETEKRRYTLIDAPGHKMYVSEMGAS 360
Qy 361 QADVGLVVISARKGEYETGPERGGQTRHALLAKTQGVNKMVWVVKMDDPTVWMSKERY 420
Db 361 QADVGLVVISARKGEYETGPERGGQTRHALLAKTQGVNKMVWVVKMDDPTVWMSKERY 420
Qy 421 DQCVSNVSNFLRAIGYNIKTVDVMPVSGYSGANLKHVDPKPCPWTGPTLLLEYLDTMN 480
Db 421 DQCVSNVSNFLRAIGYNIKTVDVMPVSGYSGANLKHVDPKPCPWTGPTLLLEYLDTMN 480
Qy 481 HVDRHINAPFMLPIAAKMKDLGTTVEGKIESGHKKKGSTLLMPNKTAVEIQNIYNENET 540
Db 481 HVDRHINAPFMLPIAAKMKDLGTTVEGKIESGHKKKGSTLLMPNKTAVEIQNIYNENET 540
Qy 541 EVDNMGCEQVKLRKIGVEEEDISPGFVLTSPPKPIKSVTFKVAQIAIVELKSIAGFS 600
Db 541 EVDNMGCEQVKLRKIGVEEEDISPGFVLTSPPKPIKSVTFKVAQIAIVELKSIAGFS 600
Qy 601 CVMHVHTAIEBVHIVKLLHLEKGTNRKSKPPAPAKGMKVIAVLETEAPVCVETYQDY 660
Db 601 CVMHVHTAIEBVHIVKLLHLEKGTNRKSKPPAPAKGMKVIAVLETEAPVCVETYQDY 660
Qy 661 POLGRFTLRDQGTIIAIGKIVKIAE 685
Db 661 POLGRFTLRDQGTIIAIGKIVKIAE 685

RESULT 4

ABP73437
ID ABP73437 standard; protein; 721 AA.

XX ABP73437;

XX 30-JAN-2003 (first entry)

XX Candida albicans essential protein SEQ ID NO 7274.

XX Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
KW signal transduction; DNA replication; cell division; growth;
KW proliferation; Candida albicans; fungicide; antifungal.


```
14
Db 212 ESKTEPAKEBEIKNOEPAEAKENVEESKVEAPTAAPVSESEPPAST-PKTEAKASKEV 270
Qy 213 PKVEDLKISESTHNTNANTSDALIKEOEVEEDVNDMFGKDHVSLIFMGHVDAG 272
Db 271 AAAAAALKVESQAKESVNTNADALKEOEQIDASIVNDMFGKDHMSLIIFMGHVDAG 330
Qy 273 KSTWGGNLLYLTGSVDKRTIEKEREAKDAGROGWYLSWMDTNNKEERNDGKTIIEVGKAY 332
Db 331 KSTWGGNLLFLTGAVDKRTVEKEREAKDAGROGWYLSWMDTNNKEERNDGKTIIEVGKSY 390
Qy 333 FETEKRYTILDAPGHKMYSEMIGGASQADVGVLVISARKGEYETGFERGGOTREHALL 392
Db 391 FETDKRYTILDAPGHKLYISEMIGGASQADVGVLVISRKRGEYEAQFERGGQSREHAIL 450
Qy 393 AKTQGVNKMVVNKMDDPTVNSKERYDQCVSNVSNFLRAIGYNIKTIVVMPVSGYSG 452
Db 451 AKTQGVNKLVVNKMDDPTVNSKERYEBCTTKLAMYLGKVGQY-KGDVLFMPVSGYTG 509
Qy 453 ANLKDHVDPKCEPWYTGPTLLLEYLDTNNVDRHINAPFMLPIAAKMKDLGTIVEGKIESG 512
Db 510 AGLKERVSKQDAPWYNGPSLLEYLDSMPLAVRKINDPMLPISCKMKDLGTIVEGKIESG 569
Qy 513 HIKGQSTLMPNKTAIVEIQNIYNETENEDVMACGQVKLRKIGVEEDISPGFVLTPS 572
Db 570 HVKKGQNLVMPNKTQEVTTIYNETEAEADSAFCGQVRLRLRGIEBEDLSAGYVLSSI 629
Qy 573 KNPISKVTKFVAQTAIVELKSIITAGSCVWHVHTAIEEVHIVKLLHKLKSGTNRKSKP 632
Db 630 NHPVKVTRFEQAIAIVELKSIITAGSCVWHVHTAIEEVTFQTLNLOKGTNRKSKA 689
Qy 633 PAFAKGMKVIAVLETAAPVCVETQYDYPOLGRTFLRDQGTIIAIGKIVKI 683
Db 690 PAFAKQGMKIIAVLETTPECIESYDDYPQLGRTFLRDQGTIIAIGKIVTKL 740

RESULT 7
ADS44300
ID ADS44300 standard; protein; 690 AA.
XX ADS44300;
XX
XX 02-DEC-2004 (first entry)
XX Bacterial polypeptide #22730.
XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX Bacteria.
XX
XX US2003233675-A1.
XX
XX 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX
XX (CAOY/) CAO Y.
XX (HINK/) HINKLE G J.
XX (SLAT/) SLATER S C.
XX (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
XX
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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

Claim 1; SEQ ID NO 22730; 122pp; English.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

Sequence 690 AA;

Query Match 46.7%; Score 1679.5; DB 8; Length 690;
Best Local Similarity 51.4%; Pred. No. 4.5e-108;
Matches 332; Conservative 109; Mismatches 148; Indels 57; Gaps 15;

Qy 68 GYQQQVNPQGG--YQQYNPQGGYQQQFPNPGGRGNYNFNNNNLCYQAGFQPSQGMS 125
Db 74 GFVPVNNIAGGYPYQYTGQ-----QNSNSPHTKSYQYQYQ-KPTGNT 117

Qy 126 LN-----DFKQKQQAAPKPK-----KTLKL-----VSSSGIKLANATKK 160
Db 118 VDEKSRVPDFSKKSPVPPKPAIPKGVLSLGGNTSAPKSTKPIISISLGTRAPTTPK 177

Qy 161 VGTKPAESDKKESEKSAETKEPTKVEEPVKKEKPVQTEKTEKSELKPVDELKI 220
Db 178 AA--PAAQSKTETPAPKVTSESTKETAAPPP---QETP--TKSADAEAKTSPAPAAAL 230

Qy 221 SESTHNTNNANVTSADALIKEOEVEEDVNDMFGGKDHVSLIFMGHVDAGKSTMGCNL 280
Db 231 KKAEEAEPATVTE-DA--TDLQNEVDQELLKDMY-GKEHVNVIFIGHVDAGKSTLGGNI 286

Qy 281 LYLTGSDKRTIEKYREAKDAGROGWYLSWMDTNNKEERNDGKTIIEVGKAYFETEKRY 340
Db 287 LFLTGMVDKRTMEKIEREAKGAKESWYLSWALDSTSEEREKKGKTVGVRAYFETEHRR 346

Qy 341 TILDAPGHKMYSEMIGGASQADVGVLVISARKGEYETGFERGGOTREHALLKTCGVNK 400
Db 347 SLLDAPGHKGYVTNNMGASQADIGVLVISARKEGFEAGFERGGQTRHEAVLARTQGINH 406

Qy 401 MVVVNNKMDPTVNSKERYDQCVSNVSNFLRAI-GYNIKTIVVMPVSGYSGANLKDHV 459
Db 407 LVVVNNKMDPESVQWSEERYKECVKLSMFLRRVAGYNSKTDVKYMPVSAITQGVKDRV 466

Qy 460 DPKECPWYTGPTLLLEYLDTNNVDRHINAPFMLPIAAKMKDLGTIVEGKIESGHKKQOS 519
Db 467 DSSVCPWYQGPSLLEYLDSMTHLERKVNAPFIPIASKYKDLGTILEGKIEAGSIKKNS 526

Qy 520 TLLMPNKTAIVEIQNIYNETENEDVMACGQVKLRKIGVEEDISPGFVLTPSNPKIKSV 579
Db 527 VLVMPIQTLEVTAIYDEADEEIESSICGQDVRLVRG-DDSQVQTYGLTSTKPNVHAT 585

Db 559 EITALICLVDKKSGKSTRFRVKQDVQVCIARLRTAGTICLETFFKDPQMGRTLRDEG 618
Qy 673 TTTAIGKIVKI 683
Db 619 KTTAIGKVLKL 629
RESULT 12
AD C35080
XX ADC35080 standard; protein; 499 AA.
AC ADC35080;
XX
DT 18-DEC-2003 (first entry)
XX Human breast cancer antigen seq id 46.
DE breast cancer; breast cancer diagnosis; breast cancer antigen.
XX Homo sapiens.
XX OS
XX US2003108888-A1.
XX PN
XX PD 12-JUN-2003.
XX PF 15-MAY-2002; 2002US-00146473.
XX PR 15-MAY-2001; 2001US-0291150P.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI Scanlan MJ, Gout I, Stockert E, Old LJ, Gure A, Chen Y;
XX WPI; 2003-829397/77.
DR N-PSDB; ADC35122.
XX
PT Diagnosing breast cancer in subject by obtaining biological sample from
PT subject, contacting sample with breast cancer-associated polypeptides,
PT determining specific binding between polypeptides and agents in sample.
XX
PS Example 2; SEQ ID NO 46; 173pp; English.
XX
CC The invention describes a method of diagnosing breast cancer in subject
CC comprising contacting biological sample from subject with at least two
CC different breast cancer-associated polypeptides (I) encoded by nucleic
CC acid molecules (II) comprising sequence chosen from 42 fully defined
CC sequences as given in specification, determining specific binding between
CC (I) and agents in sample, where presence of the binding is diagnostic for
CC breast cancer. The method is useful for diagnosing breast cancer in a
CC subject. The sample is blood, lymph node fluid or breast discharge fluid.
CC This is the amino acid sequence of a breast cancer antigen.
XX
SQ Sequence 499 AA;
Query Match 37.7%; Score 1354.5; DB 7; Length 499;
Best Local Similarity 52.5%; Pred. No. 1.2e-85;
Matches 262; Conservative 89; Mismatches 139; Indels 9; Gaps 5;
Qy 188 KVEEP-VKKEKPQTEKEEKSELPKVEDLKISESTHNNANVT SADALIKEQEEV 246
Db 2 ELSEPIVNGETEMSPESWEHKEISEAEP--GGSLGDGRPPESAHEMMEEEIP 58
Qy 247 DDEVNDMFG--KDHVSLIPMGHVDAGKSTMGNLLYLTGSDVKRTIEKYERAKDAGR 304
Db 59 KPSWVAPPAPKKEHNVVFIQHVDAKSTIGQIMYLTMGVDKRTLEKYERAKEKNR 118
Qy 305 QGWLSVMDTNKKEERNDGKTIEVGKAYFEFEKERVYTLDPAGHKMVSEMGASADY 364
Db 119 ETWLSWALDNTQBERDKGTVEGRAYFEFEKXKHFTILDAPGHKSPVNMIGASQADL 178
Qy 365 GVLVISARKGEYTGFRGGGTREHALIAKTQGVNKMVVVNNKMDPTVNMSEKRYDQCV 424

Db 179 AVLVISARKGEFETFEKGQGTREHAMLAKTAGVKHLIVLKNKMDPTVNMSEKRYBECK 238
Qy 425 SNVSNFLRAIYNIKTVDVWEPVSGYSGANLKHVDPKCEPWTGTPTLLEVLDTMNHVDR 484
Db 239 EKLVPFLKKVGFNPCKDIHFMPCSGLTGANLKQSD--FCFWYIGLFPFIPYLDNLNPNR 296
Qy 485 HINAPFMLPIAAKMKDGLTIVEGKIESGHICKGOSTLLMPNKTAVEIQNIYNETENEVD 544
Db 297 SVDPRLPIVDKYKDMGTVVLKLESGSICKGQQLVMPNKNVVLGILSD-DVETDT 355
Qy 545 AMCGEQVKLRIGKVEEEDISPGFVLTSPPKNPIKSVTKFVAQIAIIVELKSIIAAGFCVMH 604
Db 356 VAPGENLKIRLKGIEEELPGFILCDPNNLCHSGRTFDAQIIVIEHKSIIICPGYNAV 415
Qy 605 VHTAIEVHVIVKLLHLEKGTNRKSKPPAFKGMKVIIVLEAPVCVETDYDYPOLG 664
Db 416 IHTCIEVEITALICLVDKKSGKSTRFRVKQDVQVCIARLRTAGTICLETFFKDPQMG 475
Qy 665 RFTLRDQGTITIAIGKIVKI 683
Db 476 RFTLRDEGKTIAGKVLKL 494
RESULT 13
AD N03793
ID ADN03793 standard; protein; 499 AA.
AC ADN03793;
XX
DT 01-JUL-2004 (first entry)
XX
DE Antipsoriatic protein sequence #93.
XX
KW antipsoriatic; gene therapy; psoriasis; diagnosis.
XX OS Homo sapiens.
XX WO2004028479-A2.
XX PN
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030907.
XX
PR 25-SEP-2002; 2002US-0414006P.
XX (GETH) GENENTECH INC.
XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;
XX
DR WPI; 2004-305105/28.
DR N-PSDB; ADN03792.
XX
XX New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.
XX
XX Claim 9; SEQ ID NO 187; 3069pp; English.
XX
XX The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polypeptides of the invention.
XX
SQ Sequence 499 AA;
Query Match 37.7%; Score 1354.5; DB 8; Length 499;
Best Local Similarity 52.5%; Pred. No. 1.2e-85;
Matches 262; Conservative 89; Mismatches 139; Indels 9; Gaps 5;
Qy 188 KVEEP-VKKEKPQTEKEEKSELPKVEDLKISESTHNNANVT SADALIKEQEEV 246

Db	476 RFTLRDEGKTIAGKVLKL 494	
RESULT 15		
ID	ADP24765 standard; protein; 499 AA.	
XX	ADP24765	
XX	ADP24765;	
XX	18-NOV-2004 (first entry)	
DT	PRO polypeptide SEQ ID NO:1943.	
XX	PRO: antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;	
XX	osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;	
KW	antiaethmatic; hepatotropic; respiratory; gene therapy; immune system.	
KW	Unidentified.	
XX	WO2004041170-A2.	
XX	21-MAY-2004.	
XX	30-OCT-2003; 2003WO-US034312.	
XX	01-NOV-2002; 2002US-0423394P.	
XX	(GETH) GENENTECH INC.	
XX	Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WT;	
XX	Wu TD;	
XX	WPT; 2004-419628/39.	
DR	N-PSDB; ADP24764.	
XX	New PRO polypeptides and polynucleotides, useful for treating e.g.	
PT	erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated	
PT	renal disease, or demyelinating diseases of the central or peripheral	
PT	nervous system.	
XX	Claim 7; SEQ ID NO 1943; 2940pp; English.	
XX	The invention relates to a novel isolated nucleic acid and the PRO	
CC	polypeptide encoded by it. A protein of the invention has	
CC	antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,	
CC	osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,	
CC	antiaethmatic, hepatotropic, and respiratory activity. A polynucleotide	
CC	of the invention may have a use in gene therapy. The PRO polypeptide, its	
CC	agonist, antagonist, or antibody that specifically binds to the	
CC	polypeptide is useful for treating an immune related disorder such as	
CC	systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, an	
CC	juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an	
CC	idiopathic inflammatory myopathy, Sjogren's syndrome, autoimmune	
CC	vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune	
CC	thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal	
CC	disease, a demyelinating disease of the central or peripheral nervous	
CC	system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,	
CC	a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary	
CC	disease, infectious or autoimmune chronic active hepatitis, primary	
CC	biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,	
CC	inflammatory bowel disease, Gluten-sensitive enteropathy, Whipple's	
CC	disease, an autoimmune or immune-mediated skin disease, a bullous skin	
CC	disease, erythema multiforme, contact dermatitis, psoriasis, an allergic	
CC	disease, asthma, allergic rhinitis, atopic dermatitis, food	
CC	hypersensitivity, urticaria, an immunologic disease of the lung,	
CC	eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity	
CC	pneumonitis, a transplantation associated disease, graft rejection or	
CC	graft-versus-host disease. The present sequence represents a PRO protein	
CC	of the invention.	
XX	Sequence 499 AA;	

Query Match 37.7%; Score 1354.5; DB 8; Length 499;

Best Local Similarity 52.5%; Pred. No. 1.2e-85;		
Matches 262; Conservative 89; Mismatches 139; Indels 9; Gaps 5;		
Qy	188 KVEEP-VKKEEKPVQTEETEEKSELKPKVEDLKLKISESTHNTNNANVT SADALIKEQEEV	246
Db	2 ELSEPIVENGETEMSPESWEHKEEISEAEP--GGSLGDGRPEESAHEMMEEEBEIP	58
Qy	247 DDEVNDMFGG--KDHSVLI FMGHVDAGKSTMGNGNLLYLTGSDVKRTIEKYEREAKDAGR	304
Db	59 KPSVVAAPGAPKKEHVNVVFI GHVDAGKSTIGQIMYL TGMVDKRTLEKYEREAKENR	118
Qy	305 QGWYLSWVMDTNKEERNDKKTIEVGKAYFETEKRRYTILDAPGHKMYVSEMIGASQADV	364
Db	119 ETWYLSWALDTNQEERDKGTVEGRAYFETEKKHFTILDAPGHKSFVPMNIGASQADL	178
Qy	365 GVLVISARKGEYETGPERGGQTRHALLAKTQGVNKMVVVVKMDDEPTVANSKERYDOCV	424
Db	179 AVLVISARKGEFETGFEKGGQTRHAMLAKTAGVKHLIVLINKMDDEPTVANSERYBECK	238
Qy	425 SNVSNFLRAIGYNIKTDVWFMVPVSGYSGANLKHVDPKCPWYTGPTLLLEYLDTMNHVDR	484
Db	239 EKLVPFLKKVGFNPKDIHPMPCSLTGANLKEQSD--FCFWYIGLFPFIPYLDNLNPNR	296
Qy	485 HINAPFMLPIAAKMKDLGTTIVEGKIESGHKKGOSTLLMKNKTAVEIQNIYNTENEVDM	544
Db	297 SVDPRLPIVDKYKDMGTVVVLGKLESGSICKGQQLVMPKHNVEVLGILSD-DVETDT	355
Qy	545 AMGGEQVKLRIGKVEEEDISPGFVLTSPPKPIKSVTKFVAQIAIVELKSIIAAGFSCVMH	604
Db	356 VAFGENLKIRLKGIEEEIILPGFILDPNLCHSGRTFDAQIVIIHKSIIICPGYNVLH	415
Qy	605 VHTAIEBVHIVKLLHLEKGTNRKSKPPAFKGMKVIIVLETEAPVCVETYQDYPOLG	664
Db	416 IHTCIEVEITALICLVDKSGSEKSTRPFVKQDQVCIARLRITAGTICLETFFKDFPQMG	475
Qy	665 RFTLRDQGTITIAIGKIVKI 683	
Db	476 RFTLRDEGKTIAGKVLKL 494	

Search completed: July 1, 2005, 18:16:58

Job time : 197.103 secs

GenCore version 5.1.6
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OM protein - protein search; using sw model

Run on: July 1, 2005, 18:06:15 ; Search time 40.0283 Seconds
(without alignments)
1646.548 Million cell updates/sec

Title: US-09-591-632-2
Perfect score: 3594
Sequence: 1 MDSNQGNQNNYQYQSQNG.....FTLRDQGTGAIGKIVKIAE 685

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3594	100.0	685	1 EFBYS2	suppressor 2 prote
2	2177	60.6	741	2 S12921	suppressor 2 prote
3	1719	47.8	729	2 T51896	probable translati
4	1689	47.0	662	2 T41442	omnipotent nonsens
5	1675	46.6	662	2 T51948	omnipotent nonsens
6	1375	38.3	614	2 S58444	SUP35 protein - Af
7	1354.5	37.7	499	2 S06941	suppressor 2 prote
8	1283.5	35.7	515	2 T03717	GTP-binding protei
9	1213.5	33.8	573	2 T23102	hypothetical prote
10	1160.5	32.3	409	2 T03718	suppressor 2 prote
11	946.5	26.3	280	2 T43011	suppressor protein
12	859.5	23.9	435	2 A49171	translation elonga
13	847	23.6	441	2 S54734	translation elonga
14	844	23.5	456	2 S11665	translation elonga
15	836.5	23.3	449	2 A54760	translation elonga
16	833	23.2	458	2 S35894	translation elonga
17	831	23.1	458	2 A35154	translation elonga
18	829	23.1	458	2 S06300	translation elonga
19	829	23.1	460	2 S35772	translation elonga
20	828.5	23.1	449	2 JC5117	translation elonga
21	826	23.0	435	2 S43507	translation elonga
22	825.5	23.0	460	2 S43861	translation elonga
23	825	23.0	458	2 A25938	translation elonga
24	823	22.9	460	2 T41617	translation elonga
25	822.5	22.9	457	2 S35986	translation elonga
26	822	22.9	460	2 T38230	translation elonga
27	821	22.8	435	2 H90162	hypothetical prote
28	821	22.8	459	2 JC4253	translation elonga
29	819	22.8	460	2 T42089	translation elonga

30	817	22.7	460	2 T43267	translation elonga
31	814.5	22.7	460	2 JC4214	translation elonga
32	813.5	22.6	460	2 T47258	translation elonga
33	812	22.6	444	2 T44963	translation elonga
34	808.5	22.5	461	2 T43704	translation elonga
35	806.5	22.4	446	2 S16308	translation elonga
36	802	22.3	459	2 S59595	translation elonga
37	800	22.3	460	2 T43894	translation elonga
38	799.5	22.2	449	2 S08534	translation elonga
39	798.5	22.2	448	2 S10507	translation elonga
40	798.5	22.2	449	2 S06724	translation elonga
41	798.5	22.2	967	2 F86214	protein T6D22.2 [i
42	798	22.2	437	2 C72570	probable translati
43	797.5	22.2	458	1 EFBY1A	translation elonga
44	797	22.2	462	2 A60491	translation elonga
45	796.5	22.2	462	1 EBFH1	translation elonga

ALIGNMENTS

RESULT 1

EFBYS2

suppressor 2 protein - yeast (Saccharomyces cerevisiae)

N/Alternate names: G1-to-S transition protein; protein YD9395.05; protein YDR172W

C/Species: Saccharomyces cerevisiae

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C/Accession: S00733; JT0323; S49768; S00488; A26742; S00533; S05723

R/Wilson, P.G.; Culbertson, M.R.

J. Mol. Biol. 199, 559-573, 1988

A/Title: SUP12 suppressor protein of yeast. A fusion protein related to the EF-1 family

A/Reference number: S00733; MUID:88172503; PMID:3280807

A/Accession: S00733

A/Molecule type: DNA

A/Residues: 1-685 <WIL>

A/Cross-references: UNIPROT:P05453; EMBL:X07163; NID:g4581; PIDN:CAA30155.1; PID:g4582

R/Kushnir, V.V.; Ter-Avanesyan, M.D.; Telckov, M.V.; Surguchov, A.P.; Smirnov, V.N.; I

Gene 66, 45-54, 1988

A/Title: Nucleotide sequence of the SUP2(SUP35) gene of Saccharomyces cerevisiae.

A/Reference number: JT0323; MUID:88329727; PMID:3047009

A/Accession: JT0323

A/Molecule type: DNA

A/Residues: 1-685 <KUS>

A/Cross-references: EMBL:M21129; NID:gl72789; PIDN:AAA35133.1; PID:gl72791

R/Murphy, L.; Harris, D.E.

submitted to the EMBL Data Library, November 1994

A/Reference number: S49764

A/Accession: S49768

A/Molecule type: DNA

A/Residues: 1-685 <MUR>

A/Cross-references: EMBL:Z46727; NID:gl289283; PIDN:CAA86677.1; PID:gl289287; GSPDB:GN00

R/Kikuchi, Y.; Shimatake, H.; Kikuchi, A.

EMBO J. 7, 1175-1182, 1988

A/Title: A yeast gene required for the G1-to-S transition encodes a protein containing a

A/Reference number: S00488; MUID:88296422; PMID:2841115

A/Accession: S00488

A/Molecule type: DNA

A/Residues: 1-52, 'C', '54'-685 <KIK>

A/Cross-references: GB:Y00829; EMBL:Y00859; NID:g3711; PIDN:CAA68760.1; PID:g3712

C/Genetics:

A/Gene: SGD:SUP35; SUP12; GST1; SUP2; MIPS:YDR172W

A/Cross-references: SGD:S0002579; MIPS:YDR172W

A/Map position: 4R

C/Superfamily: suppressor 2 protein; translation elongation factor Tu homology

C/Keywords: duplication; GTP binding; nucleotide binding; P-loop; phosphoprotein; tandem

F:1-123/Domain: A <DOM1>

F:42-119/Region: 10-residue repeats

F:124-253/Domain: charged <DOM2>

F:159-222/Region: glutamic acid/lysine-rich

F:254-685/Domain: C <DOM4>

F:261-409/Domain: translation elongation factor Tu homology <ETU>

F:267-274/Region: nucleotide-binding motif A (P-loop)

F:406-409/Region: GTP-binding NKXD motif

A:Cross-references: EMBL:AL391572; GSPDB:GN00116; NCSP:B23111.80
A:Experimental source: BAC clone B23111; strain OR74A
C:Genetics:
A:Gene: NCSP:B23111.80
A:Map position: 6
A:Introns: 111/1; 711/3
C:Superfamily: suppressor 2 protein; translation elongation factor Tu homology

```
Query Match 47.8%; Score 1719; DB 2; Length 729;
Best Local Similarity 49.9%; Pred. No. 1.3e-81;
Matches 365; Conservative 98; Mismatches 204; Indels 64; Gaps 15;

Qy 7 GNNQNYQ-----QYSGNQOQGNRYQGYQAYNA----- 37
Db 3 GNVQNWEEAADQERLARQYQQQNNINAGTFR-PGAAAFTPGAPSPFTPGQFAAPGFTPQ 61
Qy 38 -QAQAGAGYQNY-QGYSGYQGGYQOYNPDAGYQOQYQOYNPQGGYQOYNPQGGYQOQFNQ 95
Db 62 YQOQYVGAQGGYQGGYQOYQGGYQOYNNQ-QOQGYGAVYQGGYQGGYQOQOQOQ 119
Qy 96 GGRGNY-KNFYNNNLQYQAGFQPOSQGMSLND---FQKQKQAAPK-----PKKTL--- 144
Db 120 QOYGYQOQOYQOQOQNRDAPKPAQIVKRPQPAQAQPKADAPKTAAPVKVLSVG 179
Qy 145 ----KLVSSTGKILANATKV---GTPAESDKKEEKSATETKEPTKEPVKEPVKKE 196
Db 180 GDAPAKVLISIGDAPKPAKVLISIGTAPA---KEEPEKAKEGTAABAANKVTATKAV 236
Qy 197 EKPQVTEKTEKSELPELVDLKISSEHTNNANVTSDALIKE-DEEEVDDVVDNMF 255
Db 237 QK---TESAASGRTSPAPSSGRASPAAKSGNKVSRDVADEKDIQADVDEDTLKEIY 293
Qy 256 GGDHVSILFMGHVDAGKSTGNNLLYTGSDVKRTIEKYERAKDAGRGWYLSWMDT 315
Db 294 -GKEHNIIFTHVDAGKSTLGGAILYVTGMVDQRTLDKYKREAKDMGRETWYLSWALDL 352
Qy 316 NKEERNDKTEVGVKAYPETEKRYTILDPAGHKMYSEMIGGASQADGVGLVTSARKGE 375
Db 353 TNEERAKGTEVGVGPFETDKRYSTILDAPGHYTPVNNMTGGASQADGVGLVTSARKGE 412
Qy 376 YETGFERGGQTHALLAKTGKNNKVVVNNKMDPTNWSKERYDQCVSNVSNFLRAIG 435
Db 413 YETGFEKGGQTHALLAKTGKNNKVVVNNKMDPTNWSERYKECTTKLAQFLKGTG 472
Qy 436 YNKTVDVFMVPSVSGANLKHVDPKCEPYTGTPTLLEYLDTNMHVDHINAPFMLPIA 495
Db 473 YNLKTDVFMVPAQAQMTGMIKDRVPKDLCPWYDPSLLEYLDNMSLSEKRVNAPFMAVS 532
Qy 496 AKMKDLGTIVEGKTESGHIKKGQSTLMPNKTAVEIQNIYNETENEVDMAWCGEQVKLRI 555
Db 533 KYRDMGTMBGKTEAGVIRKGMSLIMPNKQSIETSAVYGETEDEVPAQCGEQVRLRL 592
Qy 556 KGVEEEDISPGFVLTSKPNPIKSTKFAQIAIVELKSIIAAGFSCVMHVTAEVHVHIV 615
Db 593 RGIIEEIMPFGVLCSPRLVHNVTAFQAQIRILDLSILTAGNCVLHVHAAEEVTFPA 652
Qy 616 KLLHLEKGTNRKSKPPAPFAKGMKVIATLET---EAPVCVETQYDYPOLGRTFLRDQ 672
Db 653 ALLHKLQGTNRKSKLPPSHAKGDSIIARLEVTGAGGSVCVERFEDVPQMGRTFLRDQ 712
Qy 673 TTAIGKIVKI 683
Db 713 QTIAIGKITKL 723
```

RESULT 4
T41442
omnipotent nonsense suppressor, efi alpha factor-like gtp-binding protein - fission yeast
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41442
R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1998

A:Reference number: Z21993
A:Accession: T41442
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-662 <SEE>
A:Cross-references: UNIPROT:O74718; EMBL:AL032824; PIDN:CAA21821.1; GSPDB:GN00068; SPDB:
A:Experimental source: strain 972h-; cosmid c584
C:Genetics:
A:Gene: SPDB:SPCC584.04
A:Map position: 3
A:Introns: 44/1
C:Superfamily: Domain: translation elongation factor Tu homology
P:239-387/Domain: translation elongation factor Tu homology <TU>

```
Query Match 47.0%; Score 1689; DB 2; Length 662;
Best Local Similarity 48.2%; Pred. No. 4.1e-80;
Matches 342; Conservative 121; Mismatches 169; Indels 78; Gaps 17;

Qy 4 SNOGNNQNYQOYQSONGNOQGNRYQGYQAYNAQAQAGGYQNYQGYSGYQGGYQOY 63
Db 3 SNOGNNGEDEQLAKQTSKLSMSAKAPFTTPKAAFFIPS-----FQRPGFVPV 50
Qy 64 NPDAGYQOYNPQGG--YQOYNPQGGYQOQFNPQGGRGNYKNFYNNNLQGYQAGFQPS 121
Db 51 N-----NIAGYPYQYTGQ-----QNSNSPHTKSYQYQYQ-KP 85
Qy 122 QGMSLN-----DFQKQKQAAPKPK-----KTLKL-----VSSGIGILAN 156
Db 86 TGNTVDEDKSRVPDFSKKSPVPKPAIPKGVLSLGGNTSAPKSTKPIISLGGTKAPT 145
Qy 157 ATKVGCTPAESDKKEEKSATETKEPTKEPVKEPVKEPVKEPVTEKTEKSELPKVE 216
Db 146 TTKPAA--PAAQSTETTPAPKVTSSESTKETAAPP--QETP--TKSADAEALAKTPSAP 198
Qy 217 DLKISSEHTNNANVTSDALIKEQEEVDVVDNMFQGGKHVSLIFMGHVDAGKSTM 276
Db 199 AALAKKAAEAEPATVTE-DA--TDLQNEVDQELLKDMY-GKEHNVIFIGHVDAGKSTL 254
Qy 277 GGNLLYLTGSDVKRTIEKYERAKDAGRGWYLSWMDTNNKEERNDGKTIIEVGKAYFTE 336
Db 255 GGNILFLTGMDKRTMEKIEREAKESWYLSWALDSTSEEREKGTVEVGRAYFTE 314
Qy 337 KRRVTILDAPGHKMYSEMIGGASQADGVGLVTSARKGEYETGFERGGQTHALLAKTQ 396
Db 315 HRRFSLDAPGHKGYVTNNMGASQADIGVLVISARREGEFAGFERGGQTHAVLARTQ 374
Qy 397 GVNKQVNVNKMDDPTNWSKERYDQCVSNVSNFLRAI-GYNIKTVDVFMVPSVSGANL 455
Db 375 GINHLVVVNNKMDPSVQWSEERYKECVDKLSMFLRRVAGVNSKTDVKNMVPVSAITQNV 434
Qy 456 KDHVDPKCEPYTGTPTLLEYLDTNMHVDHINAPFMLPIAAKMKDLGTIVEGKIESGHIK 515
Db 435 KDRVDSVCPWYQGPSLLEYLDSMTLHLEKRVNAPFIMPIASKYKDLGTILSGKIEAGSIK 494
Qy 516 KGQSTLMPNKTAVEIQNIYNETENEVDMAWCGEQVKLRIKGVBEEDISPGFVLTSKPNP 575
Db 495 KNSNLVMPINQTLLEVTAIYDEADEEISSICGQGVRLVRG-DDSDVQTYGLTSTKNP 553
Qy 576 IKSVTKEVAQIAIVELKSIIAAGFSCVMHVTAEVHVHIVKLLHLEKGTNRKSKKPPAF 635
Db 554 VHAATFIAQIALLELPSILDTGYSCVMHHTAEVEVSFAKLLHLKDK-TNRKSKKPPMF 612
Qy 636 AKKGKVIATLETAPVCVETQYDYPOLGRTFLRDQGTITTAIGKIVKIAE 685
Db 613 ATKGMKIIAELETQTPVCMERFEDYQYMGRTFLRDQGTTVAVGKVVKILD 662
```

RESULT 5
T51948
omnipotent nonsense suppressor SUP15/erF-3 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C:Accession: T51948


```
Qy 210 SELPKVEDLKISESTHNTNANVTSADALIKEQEEVVDDEVVNDMFGGKHVSILFMGHV 269
Db 97 -----RTVVDDGTH-----KEHINMVFVGHV 118
Qy 270 DAGKSTMGNNLLYLTSVDKRTIEKYREAKDAGROGYLSWVNDTKEERNDGKTIIEVG 329
Db 119 DAGKSTIGGQLMFLTGMVDKRTLEKYREAKEKRESWYLSWCDNTDEEREKSKTVEVG 178
Qy 330 KAYPETEKRRYTLIDAPCHKRMVSEMIGGASQADVGLVVISARKGEYTFGERGGQTRFH 389
Db 179 RAYPETEKRRHPTILIDAPGHKSFPVNMIVGANQADLAVLVISARGBEFTGPDGQGQTRFH 238
Qy 390 ALLAKTOGVNMVVVNMKDDPTVNSKERYDQCVSNSVNFRAIGYNIKTDDVVFMPSVG 449
Db 239 SMLVKTAGVHLVILVNMKDDPTVKEERPEKTEGLKLPFLKLGFNPKTDITDITVPCSG 298
Qy 450 YSGANLADHDVDPKCPWYTGPTLLEYLDT-MNHVDRHINAPFMLPIAAKMKDLGTIVEGK 508
Db 299 LTGAFIKDRPTGSEGNWYSGCFIEFDVLLPSYKRDENGVRCTVAEKYSEMGTVIIGK 358
Qy 509 IESGHIKKGOSTLMPNKTAVEIQNIYNETENEVDMAVCGEQVKLRKIGVEEEDISPGFV 568
Db 359 MESGCVQKGDTLVWPNKQPVQVLQIWAQ-DVETERVAVAGDNIFKLGIEEENELQGGFI 417
Qy 569 LTSKPNPIKSVTKVAQIAVELKSIIAAGFSCVMHVHTAIEEVHI-VKLLHLKEG--- 624
Db 418 ICSPDSLAKTGRVFDPAEVLVLEHRSIIASGVSCLVHIQSAAVEEVTVKVCLLRPEELGCP 477
Qy 625 ----TN-----RKS--KKPPAFKAGMKVIAVLETE 649
Db 478 IGGTINSGDWPRPQNGLOVAFNCRTGVTIATDKTGEKKRAKFKVQDEKCIWRLLESP 537
Qy 650 APVCVETVYDQYPOLGRFLTRDQGTIIAGIKVIAE 685
Db 538 EPFVLEPFKEYPYLGRLFLTRDEGKTIAIGKVLKVE 573

RESULT 10
T03718
suppressor 2 protein homolog - common tobacco (fragment)
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03718
R;Brander, K.A.; Owttrim, G.W.; Brunold, C.
Plant Physiol. 108, 1748, 1995
A;Title: Isolation of a cDNA (EMBL X85803) encoding a putative chloroplastic isoform of
A;Reference number: Z15026
A;Accession: T03718
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-409 <BR>
A;Cross-references: UNIPROT:Q40582; EMBL:L38829; NID:g1009233; PIDN:AAA79033.1; PID:g100
A;Experimental source: strain SR1
C;Genetics:
C;Superfamily: suppressor 2 protein; translation elongation factor Tu homology
C;Keywords: GTP binding; nucleotide binding; P-loop
F;386-393/Region: nucleotide-binding motif A (P-loop)

Query Match 32.3%; Score 1160.5; DB 2; Length 409;
Best Local Similarity 55.1%; Pred. No. 4.8e-53;
Matches 220; Conservative 71; Mismatches 105; Indels 3; Gaps 2;

Qy 287 VDKETIKYEREAADAGROGYLSWVMDTNKEERNDGKTIIEVGKAYFETEKRRYTILDAP 346
Db 5 VDDRTIQKYEREAADKNRESYMAVIMDTEERVKGITVEGVAHFETDTRFTILDAP 64
Qy 347 GHKRVSEMIIGASQADVGLVVISARKGEYTFGERGGQTRFHALLAKTOGVNMVVVN 406
Db 65 GHKSYPNMISGASQADGLVVISARKGEYTFGERGGQTRFHQLAKTLGVTKLLVVVN 124
Qy 407 KMDDPTVNSKERYDQCVSNSVNFRAIGYNIKTDDVVFMPSVGSYGANLKDHDVDPKCPW 466
```

```
Db 125 KMDDPTVNSKERYDEIESKMWPFPLRSSGVNVKDVQFLPISGLGSLNLRMEKSCVPW 184
Qy 467 YTGPTLLEYLDTMNHVDRHINAPFMLPIAAKMKDLGTIVEGKIESGHIKKGOSTLLMPNK 526
Db 185 WNGFPCLFETIDAVEVPPDPNGPLRMPIDDKFDMGTVMVGKIESGSIREGDNLLVMPNK 244
Qy 527 TAVEIQNIYNETENEVDMAVCGEQVKLRKIGVEEEDISPGFVLTSPKNPITKSVTKFVAQI 586
Db 245 AAVKLAIPOD-BEKNHVGPGENVRVRLSGVEEDDILSGFVLSVAKPHAVTEFVAQL 303
Qy 587 AIVEL--KSIIAAGFSCVMHVHTAIEEVHI-VKLLHLKEGTNRKSKPPAPAKGMKVIA 644
Db 304 QILLELDNAIFTAGYKAVLHSHVSECEIVELMQQIDLTKTKPKMKKPLFVKNGAIVLC 363
Qy 645 VLETEAPVCVETVYDQYPOLGRFLTRDQGTIIAGIKVIA 683
Db 364 RVQVNNLICVEKFSDFQAQLGRFLTRTEGKTVAVGKITAL 402
```

RESULT 11

T43011

suppressor protein homolog - fission yeast (Schizosaccharomyces pombe) (fragment)
C;Species: Schizosaccharomyces pombe
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43011
R;Yoshiohka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A;Reference number: Z17323; MUID:98162722; PMID:9501991
A;Accession: T43011
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-280 <YOS>
A;Cross-references: UNIPROT:P78857; EMBL:D89207; NID:g1749621; PIDN:BAA13868.1; PID:g174
A;Experimental source: strain PR745
C;Superfamily: suppressor 2 protein; translation elongation factor Tu homology

```
Query Match 26.3%; Score 946.5; DB 2; Length 280;
Best Local Similarity 59.9%; Pred. No. 3.5e-42;
Matches 169; Conservative 56; Mismatches 54; Indels 3; Gaps 3;

Qy 405 VNKMDDPTVNSKERYDQCVSNSVNFRLAI-GYNIKTDDVVFMPSVGSYGANLKDHDVDPKE 463
Db 1 INKMDDSFQVQSESNKECVDKLSMFLRRVAGYNSKTDVKYMPVSAITGQNVKRDVSSV 60
Qy 464 CPWYTGPTLLEYLDTMNHVDRHINAPFMLPIAAKMKDLGTIVEGKIESGHIKKGOSTLLM 523
Db 61 CPWYQGPSLLEYLDSMTHLERKVNAPFIMPITASKYKDLGTILEGKIEAGSIKKNSNVLM 120
Qy 524 PNKTAVEIQNIYNETENEVDMAVCGEQVKLRKIGVEEEDISPGFVLTSPKNPIKSVTKFV 583
Db 121 PINQTLSEVTAIYDEADEIESSICGQDQVRLVRG-DDSDVQGTGYVLVTSKNPVAHTTRFI 179
Qy 584 AQIAVELKSIIAAGFSCVMHVHTAIEEVHI-VKLLHLKEGTNRKSKPPAPAKGMKVIA 643
Db 180 AQIALELPILITGYSVWHIHTAVEEVSFAKLLHLKDK-TNRKSKPPMPFATGKMKII 238
Qy 644 AVLETEAPVCVETVYDQYPOLGRFLTRDQGTIIAGIKVIAE 685
Db 239 AELETQTPVCWERFEDYQWGRFTLRDQGTITVAVGVKVKILD 280
```

RESULT 12

A49171

translation elongation factor eEF-1 alpha chain - Tetrahymena pyriformis
N;Alternate names: 14-nm filament-associated protein
C;Species: Tetrahymena pyriformis
C;Date: 21-Jan-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
C;Accession: A49171; B49171
R;Kurasawa, Y.; Numata, O.; Kato, M.; Hirano, H.; Chiba, J.; Watanabe, Y.
Exp. Cell Res. 203, 251-258, 1992
A;Title: Identification of Tetrahymena 14-nm filament-associated protein as elongation f

A;Reference number: A49171; MUID:93049915; PMID:1385189

A;Accession: A49171

A;Molecule type: mRNA

A;Residues: 1-435 <KUR>

A;Cross-references: UNIPROT:Q04634; GB:D11083; NID:g217407; PIDN:BA001856.1; PID:g217408

A;Note: sequence extracted from NCBI backbone (NCBIN:117509, NCBIPI:117510)

A;Accession: B49171

A;Molecule type: protein

A;Residues: 2-21 <KU2>

C;Genetics:

A;Genetic code: SGC5

C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog

C;Keywords: GTP binding; nucleotide binding; P-loop; protein biosynthesis

F;2-435/Product: translation elongation factor eEF-1 alpha chain #status experimental <B

F;9-157/Domain: translation elongation factor Tu homology <ETU>

F;15-22/Region: nucleotide-binding motif A (P-loop)

F;95-98/Region: GTP binding #status predicted

F;154-157/Region: GTP binding #status predicted

Query Match 23.9%; Score 859.5; DB 2; Length 435;

Best Local Similarity 39.9%; Pred. No. 2e-37;

Matches 174; Conservative 91; Mismatches 154; Indels 17; Gaps 7;

Qy 256 GGDHVSILFMGHVDAGKSTMGNNLLVLTGSVDKRTIEKYEREAKDAGRGQWYLSWMDT 315

Db 4 GDRVHINLVIGHVDGKSTTTGHLIYKCGIDKRVIEKPEKSAEQGSKFYAWVLDK 63

Qy 316 NKEBRNDGKTIEVGKAYFETEKRRYTIIDAPGHKMYVSEMIGGASQADVGVLVISARKGE 375

Db 64 LKAERERGITDISLWKFFETAKYHFTIIDAPGHRDFIKNMITGTSQADVAITMIASPGQE 123

Qy 376 YETFERGGQTRHALLAKTQGVNKMVVVNKMDPTVNWSKERYDQCVSNVSNFLRAIG 435

Db 124 FEAGISKGQGTREHALLAFTLGVRQMVCLNKMDKTVNFSEERYQBIKKELSDYLKKG 183

Qy 436 YNIKTDVVPVSGVSGANLKHVDPKCEPMTYTGPTLLVLDTMNVDHINAPFMLPI- 494

Db 184 YKPDTP-IPFIPISFGNDMLIER--STNAPWYKGPILLVEALDLEPPKRPVDKPLRLPLQ 240

Qy 495 -AAKMDLGTIVVEGKIESGHIKKQSTLLMPNKTAVEIQNIYNETENEVDMAKGEQVKL 553

Db 241 DVYKIGIGTVPGRVETGVKPGMSIQFAPNKVIAECKSVEMHHE-QLPEAVPGDNVGF 299

Qy 554 RIKGVEEDISPGFVLTPSPKN-PIKSVTKFVAQIAIVELKSIIAAGFSCVMHVHTA- 608

Db 300 NIKGVSKDIRRGVNVASDAKNDPAKEAATFYSQVIIMHPQIQIAGVTPVLDCHTAHAC 359

Qy 609 -IEEVHIVKLLKLEKGTNRKSKPPAFKGMKVIADVLEAPVCVETDYDYPOLGRFT 667

Db 360 KFETIH-----DKIDRRTGKSEQENPKFKNGDAALVTLIPTKALCDEVFQEPPLGRYA 414

Qy 668 LRQDGTIIAIGKIVKI 683

Db 415 VRDMKQIVAVGVIKV 430

RESULT 13

S54734

translation elongation factor aEF-1 alpha chain - Desulfurococcus mobilis

C;Species: Desulfurococcus mobilis

C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 02-Feb-2001

C;Accession: S54734; S38464

R;Ceccarelli, B.; Bocchetta, M.; Creti, R.; Sanangelantonio, A.M.; Tiboni, O.; Cammarano,

Mol. Gen. Genet. 246, 687-696, 1995

A;Title: Chromosomal organization and nucleotide sequence of the genes for elongation fa

obilis.

A;Reference number: S54733; MUID:95206243; PMID:7898436

A;Accession: S54734

A;Molecule type: DNA

A;Residues: 1-441 <CEC>

A;Cross-references: EMBL:X73582

A;Note: the authors translated the initiation codon GTG for residue 1 as Val

C;Genetics:

A;Gene: tuf

A;Start codon: GTG

C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog

C;Keywords: GTP binding; nucleotide binding; P-loop; protein biosynthesis

F;12-160/Domain: translation elongation factor Tu homology <ETU>

F;18-25/Region: nucleotide-binding motif A (P-loop)

F;157-160/Region: GTP-binding NKXD motif

Query Match 23.6%; Score 847; DB 2; Length 441;

Best Local Similarity 39.2%; Pred. No. 8.9e-37;

Matches 168; Conservative 99; Mismatches 154; Indels 8; Gaps 5;

Qy 258 KDHVSLIFMGHVDAGKSTMGNNLLVLTGSVDKRTIEKYEREAKDAGRGQWYLSWMDTNK 317

Db 9 KPHLNIUVIGHVDGKSTMTGHLIYRLGYFDEKTVKMIIEESKKKESKPFALLDRMK 68

Qy 318 EERNDGKTIIEVGKAYFETEKRRYTIIDAPGHKMYVSEMIGGASQADVGVLVISARKGEYE 377

Db 69 EERERGVTISLSYMKFFETKYFFTIIDAPGHRDFVKNMITGASQADAAAILVVSARKGEFE 128

Qy 378 TGFERGGQTRHALLAKTQGVNKMVVVNKMDPTVNWSKERYDQCVSNVSNFLRAIGYN 437

Db 129 AGMSAEGQTRHALLARTMGINQLIVAINKMDATEPPYSEKRYNEIKELGKFLKGLGYD 188

Qy 438 IKTDVVPVSGVSGANLKHVDPKCEPMTYTGPTLLVLDTMNVDHINAPFMLPI--A 495

Db 189 V-SKIPFIPISAMTGENLIER--SPNMPWYNGPPLVLEALDTLEVPPPKPINKPLRIPIQDV 245

Qy 496 AKMKDLGTIVVEGKIESGHIKKQSTLLMPNKTAVEIQNIYNETEN-EYDMAKCGEQVKLR 554

Db 246 YNTSIGVPGRVETGVKVGDKLVFMPAGLVAEVKTI--ETHHTKIEKAEFGDNIGPN 303

Qy 555 IKGVEEDISPGFVLTPSPKNPIKSVTKFVAQIAIVELKSIIAAGFSCVMHVHTAIEEVHI 614

Db 304 VKGVEKDKIRGVDAGSLDVPPTVADEFARIMVMHPTAIAVGTPVIHVHTASVACRI 363

Qy 615 VKLLKLEKGTNRKSKPPAFKGMKVIADVLEAPVCVETDYDYPOLGRFTLRDQGT 674

Db 364 TEITAKIDPRTGKEIEKNPHFLKQGDIAIVKFKPIKPLVWEKYSDFQGLGRFAMRDMGKT 423

Qy 675 IAIGKIVKI 683

Db 424 IGIQVLEI 432

RESULT 14

S11665

translation elongation factor eEF-1 alpha chain - slime mold (Dictyostelium discoideum)

N;Alternate names: actin-binding protein ABP-50

C;Species: Dictyostelium discoideum

C;Date: 12-Feb-1993 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004

C;Accession: S11665; S36934; S36935

R;Yang, F.; Demma, M.; Warren, V.; Dharmawardhane, S.; Condeelis, J.

Nature 347, 494-496, 1990

A;Title: Identification of an actin-binding protein from Dictyostelium as elongation fac

A;Reference number: S11665; MUID:91015340; PMID:2215665

A;Accession: S11665

A;Molecule type: mRNA

A;Residues: 1-453 <YAN>

A;Cross-references: UNIPROT:P18624; EMBL:X55973; NID:g7274; PIDN:CAA39443.1; PID:g7275

A;Experimental source: strain AX-3; clone 50-1.7

A;Accession: S36934

A;Molecule type: mRNA

A;Residues: 7-456 <YAW>

A;Cross-references: EMBL:X55972; NID:g7276; PIDN:CAA39442.1; PID:g7277

A;Experimental source: strain AX-3; clone 50-1.5

A;Accession: S36935

A;Molecule type: protein

A;Residues: 9-17;138-149;162-166;418-421 <YAF>

C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog

C;Keywords: actin binding; blocked amino end; GTP binding; nucleotide binding; P-loop; p

F;11-159/Domain: translation elongation factor Tu homology <ETU>

F;17-24/Region: nucleotide-binding motif A (P-loop)

F:156-159/Region: GTP-binding NKXD motif

Query Match	23.5%	Score	844;	DB	2;	Length	456;		
Best Local Similarity	41.0%;	Pred. No.	1.3e-36;						
Matches	176;	Conservative	82;	Mismatches	161;	Indels	10;	Gaps	6;

Qy	258	KDHVSLTFMGHVDAGKSTMGNLLYLTSQVDRKRTIEKYEREAKDAGQGWLSWMDTNK	317
Db	8	KTHINIVIGHVDAGKSTTTGHLIYKCGGIDKRVIEKYEKASEGWQSFKYAWMDKLK	67
Qy	318	BERNDGKTIEVGKAYFTEKKRYTILDAPGHKMTVSEMI GASQADVGVILVISARKEYE	377
Db	68	AERERGITIIDALWKFFSKYFTIIDAPGHRDFIKNMITGTSQADCAVLIASPTGEFE	127
Qy	378	TGPERGGOTREHALLAKTQGVNKMVWVVKMDDPTVNKSKERYDQCYSNVSNFURALTCYN	437
Db	128	AGIAKNGQTRHALLAYTLGVKQMI VAINKMDKSTNYSQARYDEIVKEVSSFFIKKTCYN	187
Qy	438	IKTDVPMPSVSGSGANLKHVDPKCEPWTGPTLLLEYLDTMNHVDRIHINAPFLMPI--A	495
Db	188	-PEKVAFPVPSIGMNGDNMLERSDKWE--WYKGPITLLEALDAIVPEKPRHDKPLRIPLQDV	244
Qy	496	AKMKDLGITVEGKLESCHI KKGQSTLLMPNKTAVEIQNIYNETENEVDMAKCGQVKLRI	555
Db	245	YKGGITGVPVGRVETGIIIPGMVVVTPAPGLSTEVKSVEMHHE-QUPEARPGNVGENV	303
Qy	556	KGVEEEDISPGFVLTSPTKN-PIKSVTKFVAQIAIVELKSI IAAGFSCVMHVHTAIEBVHI	614
Db	304	KNVSVEKIKRGMVAGDSKNDPPQETEFKFAQVILNHPGQIHAGYSVPLVDCHTAHIACKF	363
Qy	615	VKLLHLEKGTNRKSKPPAPFA--KKGKMKVIAVLETAEPVCVTEYODYPOLGRFTLRDQ	671
Db	364	TEIVDKVDRRTIGAVAKEGTAAVVLKNGDAAWELTFSRPMCVESFTEYPPGLGRFAVRDM	423
Qy	672	GTTHAIGKI	680
Db	424	ROTVAVGVI	432

RESULT 15

A54760 translation elongation factor eEF-1 alpha chain - Trypanosoma brucei
C:Species: Trypanosoma brucei
C:Date: 28-Oct-1994 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C:Accession: A54760; C49394
R:Kaur, K.J.; Ruben, L.
J. Biol. Chem. 269, 23045-23050, 1994
A:Title: Protein translation elongation factor-1alpha from Trypanosoma brucei binds calmodulin
A:Reference number: A54760; MUID:94364999; PMID:8083206
A:Accession: A54760
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-239, 'TCT', 243-449 <KAU>
A:Cross-references: UNIPROT:P41166; GB:U10562; NID:g507782; PIDN:AAA57476.1; PID:g507783
R:Baldauf, S.L.; Palmer, J.D.
Proc. Natl. Acad. Sci. U.S.A. 90, 11558-11562, 1993
A:Title: Animals and fungi are each other's closest relatives: congruent evidence from m
A:Reference number: A49394; MUID:94089672; PMID:8265589
A:Accession: C49394
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 18-415 <BAL>
A:Cross-references: R125868; NID:g438909; PIDN:AAA16602.1; PID:g438910
C:Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog
C:Keywords: calmodulin binding; GTP binding; nucleotide binding; P-loop
F:8-156/Domain: translation elongation factor Tu homology <ETU>
F:14-21/Region: nucleotide-binding motif A (P-loop)
F:153-156/Region: GTP-binding NXKD motif

Query Match	23.3%	Score 836.5;	DB 2;	Length 449;
Best Local Similarity	39.9%	Pred. No. 3.2e-36;		
Matches 172; Conservative	88;	Mismatches 164;	Indels 7;	Gaps 5;

258	Qy	KDHVSLIFPMGHVDAGKSTMGNLLYLTGSDVDRKPTIEKYERAKDAGROGWLSWMDTNK	317
Db	5	KVHMNLVVVGHVDAGKSTAGHLTYKCGGIDKRTIEKFEKAADTGKASFYAWVLDDKLK	64
Qy	318	EERNDGKTIIEVGRAYFETEKRRYITILDAPGHKMVSEMIGASQADVGVLVTSARKGEYE	377
Db	65	AERERGITIDIALWKFPSPKSVFTIIDAPGHRDFPKMWTGTSQDAAILIITASQGEFE	124
Qy	378	TGFERGGQOTREHALLAKTQGVNKMVVVNKNMDDPTVNMKRGYDQCVSNVSNFLRAIGNV	437
Db	125	AGISKQGTREHALLAFTLGVQVMVVCNKMDDKTVNYGQERYDBIIVKEVSAYIKKGVN	184
Qy	438	IKTDVVPMPVSGYSGANLKHVDKPECPWYTGPTLLEVLDTMNVHNRHINAPFMLPI--A	495
Db	185	VE-KVRVPIPSGGQDNNIE--KSEKMPWYKGPLLEALDMLDPPVRPSDKPLRPLQDV	241
Qy	496	AKMKDLGTIVEGKIESGHIKKGGQSTLMPNKTAVEIQINYNETENEVDMMACGEQVQLRI	555
Db	242	YKIGGIGTVPGRVETGVMKPGDVVTFAPANVTTEVKSIEMHHE-QLAEAETPGDNGFNV	300
Qy	556	KGVEEEDIISGFVLTSFN-PIKSVTFKVAQIAIVELKSIIITAGFSCVMHVHTATEEVHI	614
Db	301	KNVSVKDIRRGVCGNTKNDPPKEAADFTAQVITLNPQGQINGYAPVLDCHTSHIACKF	360
Qy	615	VKLLHLKEKGTNRKSKPPAPFAKGMKVIAVLETPAPVCVETVODYPOLGRFTLRDQGT	674
Db	361	AEIESKIDRRSGKELEKAPKSIKSGDAIIVRMVPQKPMCEVFENDYAPLGRFVDRMQT	420
Qy	675	IAIGKIVKIAB	685
Db	421	VAVGIIKAVTK	431

Search completed: July 1, 2005, 18:20:58
Job time : 42.0283 secs

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OM protein - protein search, using sw model

Run on: July 1, 2005, 18:17:24 ; Search time 50.3582 Seconds
(without alignments)
1015.419 Million cell updates/sec

Title: US-09-591-632-2

Perfect score: 3594

Sequence: 1 MSDSNQGNQNIQQYQSQNG.....FTLRDQGTIAIGKIVKIAE 685

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgm2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgm2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgm2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgm2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgm2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
- 6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1365.5	38.0	714	4	US-09-949-016-11158
2	1307.5	36.4	499	2	US-08-820-170A-40
3	1307.5	36.4	499	3	US-09-055-699-40
4	1307.5	36.4	499	3	US-09-273-565-40
5	1307.5	36.4	499	3	US-09-565-538-40
6	1307.5	36.4	499	3	US-09-661-468-40
7	1307.5	36.4	499	4	US-09-976-165-40
8	1072.5	29.8	276	4	US-09-248-796A-19828
9	831	22.3	460	4	US-09-248-796A-19819
10	801.5	22.3	462	1	US-08-299-351-1
11	799.5	22.2	460	3	US-09-174-768-4
12	797.5	22.2	469	4	US-09-949-016-9570
13	797.5	22.2	469	4	US-09-949-016-9571
14	796.5	22.2	462	4	US-09-309-572-10
15	796.5	22.2	462	4	US-09-718-096-10
16	796.5	22.2	462	4	US-09-949-016-6075
17	796.5	22.2	462	6	5225348-1
18	796.5	22.2	462	6	5225348-1
19	796.5	22.2	469	4	US-09-949-016-7704
20	788.5	21.9	462	2	US-08-371-377-18
21	788.5	21.9	462	4	US-08-875-553D-24
22	778.5	21.7	478	4	US-09-949-016-7819
23	593.5	16.5	398	2	US-08-371-377-17
24	593.5	16.5	398	2	US-08-875-553D-23
25	589	16.4	397	2	US-08-371-377-19
26	589	16.4	397	4	US-08-875-553D-25
27	473.5	13.2	204	4	US-09-248-796A-19818

US-09-949-016-11158
; Sequence 11158, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11158
; LENGTH: 714
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11158

Query Match 38.0%; Score 1365.5; DB 4; Length 714;
Best Local Similarity 50.9%; Pred. No. 4.4e-111;
Matches 267; Conservative 94; Mismatches 155; Indels 9; Gaps 5;

Qy 162 GTPAESDKEEKSAAETKPTKEPTKVESP-VKKEKPVOTEKTEKSELPKVEDLKI 220
Db 191 GGRAAPVSSQEEQSCEGNSAVSMELSPVINGTENGSPESWEHEKISEAEP--- 247
Qy 221 SESTHTNNANVTSSADALIKEQEEVEVDDEVVNDMFGG--KDHVSLIFMGHVDAGKSTWG 278
Db 248 GGGSLGDRPPEESAHEMEEEBEIPKPSVAPPAPKKEHVNVVFIGHVDAGKSTTGG 307
Qy 279 NLLYLTGSDVKTTEKYEKADAGROGWLSWMDNKEBNDGKTIKVEKAYFETEKR 338
Db 308 QIMYLTGMVDKRTLEKYEKAKENRETWYLSWALDNTQEEERDKGTVEVGRVFPETKK 367
Qy 339 RYTILDAPGHVMYSEMIGASQADGVLVTSARKGEVETGFERGGOTREHALLAKTQGV 398
Db 368 HFTILDAPGHKSFPVNMIGASQADLAVLVISARKGEFETGFGGQTRHAKLAKTAGV 427
Qy 399 NKMMVVVNMDDPTVNMNSKERYDQCVSNVSNFLRAIGNIKTVDVFMVPSGYSANLKH 458
Db 428 KHLIVLNMDDPTVNMNSERYBECKELVFLFKKGVFNPKDHFMPKSGLTGANLKEQ 487
Qy 459 VDPKECPWYGTPTLLELYDTWNHVRHINPFMLPIAAKMDLGTIVEGKTESGHKKGO 518

ALIGNMENTS

RESULT 1

US-09-949-016-11158
; Sequence 11158, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11158
; LENGTH: 714
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11158

Qy		238	L I K Q E B -- E V D D E V N D M F G G K O H V S L P M G H V D A G K S T W G N L N Y L T G S V D K R T I E K Y	295
Db		50	M M E E K E J R K S V I P S G P A K C H E V N V P T G H V D A G K S T I G G Q I M F T G M A D K R T L E K Y	109
Qy		296	E R E A K D A G R O Q W I L S W N M D T N K E E R N D G K T I E V G K A Y P E T E K R R Y T I L D A P G H K W V S M	355
Db		110	E R E A E K N R E T W Y L S W A L D T W Q E E R D K C K T V E G R A Y P E T E R K H F T I L D A P G H K S F V P N M	169
Qy		356	I G G A S O A D V G V L V T S A R K G E Y E T F P E R G O Q T R E H A L L A K T Q V N K M V V V N K O M D P T V N W	415
Db		170	I G G A S O A D L A V L V T S A R K G E F E T F E G K G O T R E H A M F G K T A G V K H L I V L I N K O M D P T V N W	229
Qy		416	S K E R Y D O C V S N V S N F L R A I G Y N I K T D V V F M P V S G Y S G A N L K D H V D K E C P W T Y G T T L E Y	475
Db		230	G I E R Y E C K E K L V P F L K V G S P K D I H F M P C S G U T G A N I K E Q S D - F C P W T Y G L P F P T Y	287
Qy		476	L D T M N H V D R H I N A P M F L P I A A K M D L G T I V E K G I E S G H I K K G Q S T L L M P N K T A V B I O N Y	535
Db		288	L N N L P N F N R S I D G P T R L P I V D K Y X M G T V W L G K L B S S I F K G Q L W M P N K H N V E L G I L	347
Qy		536	N E T E N E V D M A M C E Q V K L R I K G V E E E D I S P G F V L T S P K N P I K S V T K F V A Q I A I V E L K S T I	595
Db		348	S D - D T E T D F V A P G G N L K I R L G I E E E E L P F I L C D P S N L C H S G R T F D Q V I I I S H K S I I	406
Qy		596	A A G P S C V M H V T A I E E V H I V L L H K L E K G T N R K S K P A F A K M G M V A I V E T E A P C V E	655
Db		407	C P G Y N A V L I H T C I E E V E I T A L I S I V D K K S G E K S T R P R F V K Q D O V C I A R L F T A G T I C L E	466
Qy		656	T Y Q D Y P O L G R P T L R D Q G T T I A I G K I V K I	683
Db		467	T F K D F P O M G R E T L R D E G T I A I G K V L K I	494

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RESULT 4
US-09-273-565-40
; Sequence 40, Application US/09273565A
; Patent No. 6166190
; GENERAL INFORMATION:
; APPLICANT: FUJIWARA, TSUTOMU
; APPLICANT: WATANABE, TAKESHI
; APPLICANT: HORIE, MASATO
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
; TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBQUITIN-CONJUGATING ENZYME
; FILE REFERENCE: Q-5399
; CURRENT APPLICATION NUMBER: US/09/273,565A
; CURRENT FILING DATE: 1999-03-22
; EARLIER APPLICATION NUMBER: 09/055,699
; EARLIER FILING DATE: 1998-04-07
; EARLIER APPLICATION NUMBER: 08/820,170
; EARLIER FILING DATE: 1997-03-19
; EARLIER APPLICATION NUMBER: JP 63410/1996
; EARLIER FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: JP 69163/1997
; EARLIER FILING DATE: 1997-03-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-273-565-40

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Query Match      36.4%; Score 1307.5; DB 3; Length 499;
Best Local Similarity 49.4%; Pred. No. 3.1e-106;
Matches 251; Conservative 94; Mismatches 146; Indels 17; Gaps 5;

Qy 178 ETKEPTKEPTKVKEEKPVOTEKTEEKSELPKVEDLKISEHTNTNNANVTGADA 237
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Db 2 ELSEPVVENGVE-----MALESSWEHSKEVSEAEPP---GGSGSGDGPPEESGQE 49

Qy 238 LIKEQEE--EVDDEVDNDMFGGKHVSLIPMGHVDAKSTWGGNLLYLTGSVDKRTTEKY 295
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 50 MMBEKEEIRKSKSVIPVSGAPKKEHVNVFTIGHVDAGKSTIGGOIMFTGMADKRTLEKY 109
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296	Qy	296	EREKADAGROGWIYLSWMDTNKBERNDOKTTEVGKAYFETEKRRVETIILDAPGHKMVYSEM	355
110	Db	110	EREABEKNETTIIYLSWALDITNQESRDKGTVEVGRAYFETERKHPTIILDAPGHKSFVNN	169
356	Qy	356	IGGASQADVGVLVTISARKGEYETGFERGGQTRHALLAKTOGVNKMVVVVNKKMDDPTVM	415
170	Db	170	IGGASQADLAVLVTISARKGEFETGFEKGGQTRHAMPKGTAGVKHLIVLINKMDDPTVM	229
416	Qy	416	SKERYDQCVSNVSNFLRAIGNIKTDVVVMPVSGVSGANLKDHPVDKPCPWYTGPTLLEY	475
230	Db	230	GIERYECKELVPFLKKVGFSPKKD IHFMPCSGLTGANIKEQSD--PCPMWYTGLPPIFY	287
476	Qy	476	LDTMNVHVRHINAPFMLPIAAKMKDLGTHVEGKTESGHIKKGQSTLLMPNKTAVEIQNIY	535
288	Db	288	LNNLPNFRSIDGRIPLPVDKYKDMGTWVLGKLESSEGI FKQQLVMMPNKENVEVLGIL	347
536	Qy	536	NETENEDVMAACGSOVKRLIRKIGVEEEDISPGFVLTS PKNPIKSVTKFVAQIAIVELKSI	595
348	Db	348	SD-DTETDVFVAPGNNLKLRLKIGIEEELPLPFILCDPSNLCHSGRTFDVQIVLIEHKS	406
596	Qy	596	AAGFSCVMVHHTALEEVHIVKLLHKLKGTNRKSKKPAPFAKKGMKVIAVLETEAPVCVE	655
407	Db	407	CPGYNVLIHTCIEEVEITALISLVDKSKSEKSKTRPRFVKQDQVCIARLRTAGTICLE	466
656	Qy	656	TYQDYPOLGRPTLRDQGTIIAIGKIVKI	683
467	Db	467	TFKDFPQWGRPTLRDEGKTTAIGKVLK	494

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RESULT 5
US-09-565-538-40
; Sequence 40, Application US/09565538
; Patent No. 6333404
; GENERAL INFORMATION:
; APPLICANT: FUJIWARA, TSUTOMU
; APPLICANT: WATANABE, TAKESHI
; APPLICANT: HORIE, MASATO
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
; TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBQUITIN-CONJUGATING ENZYME
; FILE REFERENCE: Q-53599
; CURRENT APPLICATION NUMBER: US/09/565,538
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 09/273,565
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 09/055,699
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/820,170
; PRIOR FILING DATE: 1997-03-19
; PRIOR APPLICATION NUMBER: JP 63410/1996
; PRIOR FILING DATE: 1996-03-19
; PRIOR APPLICATION NUMBER: JP 69163/1997
; PRIOR FILING DATE: 1997-03-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-538-40

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Query Match      36.4%; Score 1307.5; DB 3; Length 499;
Best Local Similarity 49.4%; Pred. No. 3.1e-106;
Matches 251; Conservative 94; Mismatches 146; Indels 17; Gaps 5

Qy      178 ETKEPTKPEPKVVEPVKKESKPQTEBKTETKESLPKVKEDLKISESTHTNNANVTSDA 237
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Db      2 ELSEPPVNGEVE-----NALESSWEHSKEVSEAEF---GGGSSGDSPPEESQCE 49

Qy      238 LIKQEER--EVDDEVNNDMEFGGHKHUSLI PMGHVDACKS TWGNGLLYLTGSVDKRRTIEKY 295
        ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      50 MBEKEIRKSXSVIYSGAPKEHVNVFTIGHVDAGSKTGTGGOIMFTIGMADKRTLLEY 109
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Db 110 EREAENKRETWYLSWALDNTQBERDKGKTVEUGRAYFETERKHFTTILDAPGHKSFVPNM 169
Qy 356 IGGASQADVGLVTSARKGEYETFERGGQTRHALLAKTQGVNKMVWVVMKMDPTVNW 415
Db 170 IGGASQADLAVLTSARKGEFETGFKGGQTRHAFMGKTAGVKHLVLINKMDPTVNW 229
Qy 416 SKERYDOCVSNVSNFLRAIGNIKTDVFMVPSVSGANLKHVDHPKCEPMYTGPTLLEY 475
Db 230 GIERYECKEKLVPFLKKVGFSPKKDTHFMPCSGLTGANIKEQSD--FCPWTYGLPIFY 287
Qy 476 LDTMNHVDRHINAPFMLPIAAKMDLGTIVGKTESGHIKKGQSTLLMPNKTAVEIQNIY 535
Db 288 LNNLPNFRSIRIDGPIRLPIVDKYDMGTIVLKGLESIGIFKQQLVMMPNKHNVEVLGIL 347
Qy 536 NETENEVDMAWCGEQVKLRIRKGVBEEDIISPGFVLTSKPNPIKSVTKVAQIAIVELKSII 595
Db 348 SD-DTETDFVAPGENLKIRLKGIEEBEILPEFILCDPSNLCHSGRTDPDQIVIIIEHKSII 406
Qy 596 AAGFSCVMHVTATEEVHIVKLHLKLEKGTNRKSKPPAPFAKGMKVIAVLETEAPVCVE 655
Db 407 CPGYNAVLHIHTCIEEVEITALISLVDKSGEKSKTRPRFVKQDQVCIARLTAGTICLE 466
Qy 656 TYQDYPOLGRFTLRDQGTIIAIGKIVKI 683
Db 467 TFKDFPQWGRFTLRDEGKTTAIGKVLKL 494
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RESULT 6

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US-09-661-468-40
; Sequence 40, Application US/09661468
; Patent No. 6376189
; GENERAL INFORMATION:
; APPLICANT: FUJIWARA, TSUTOMU
; APPLICANT: WATANABE, TAKESHI
; APPLICANT: HORIE, MASATO
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
; FILE REFERENCE: Q-53599
; CURRENT APPLICATION NUMBER: US/09/661,468
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 09/055,699
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/820,170
; PRIOR FILING DATE: 1997-03-19
; PRIOR APPLICATION NUMBER: JP 63410/1996
; PRIOR FILING DATE: 1996-03-19
; PRIOR APPLICATION NUMBER: JP 69163/1997
; PRIOR FILING DATE: 1997-03-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-661-468-40
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Query Match 36.4%; Score 1307.5; DB 3; Length 499;
Best Local Similarity 45.4%; Pred. No. 3.1e-106;
Matches 251; Conservative 94; Mismatches 146; Indels 17; Gaps 5;
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Qy 178 ETKEPTKEPTKVEBPVKKEEKPVQTEKTEKSELKPVEDLKISESTHNTNNAVTSADA 237
Db 2 ELSEPVEVEGE-----MALESWEHSKEVSEAEPP---GGSGSDSGPPEESQGE 49
Qy 238 LIKEQEE--EVDDEVNDMFGKDHVSLIFMGHVDAGKSTMGGNLLYLTGSDVKRTIEKY 295
Db 50 MMEKEEIRKSKSVIVPSGAPKKEHVNVFVIGHVDAGKSTIGGIMFLTGMADKRTIEKY 109
Qy 296 EREKADAGROGWYLSWMDTNKEERNDGKTIEVGKAYFETEKRRYTTILDAPGHKMYVSEM 355
Db 110 EREAENKRETWYLSWALDNTQBERDKGKTVEUGRAYFETERKHFTTILDAPGHKSFVPNM 169
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Qy 356 IGGASQADVGLVTSARKGEYETFERGGQTRHALLAKTQGVNKMVWVVMKMDPTVNW 415
Db 170 IGGASQADLAVLTSARKGEFETGFKGGQTRHAFMGKTAGVKHLVLINKMDPTVNW 229
Qy 416 SKERYDOCVSNVSNFLRAIGNIKTDVFMVPSVSGANLKHVDHPKCEPMYTGPTLLEY 475
Db 230 GIERYECKEKLVPFLKKVGFSPKKDTHFMPCSGLTGANIKEQSD--FCPWTYGLPIFY 287
Qy 476 LDTMNHVDRHINAPFMLPIAAKMDLGTIVGKTESGHIKKGQSTLLMPNKTAVEIQNIY 535
Db 288 LNNLPNFRSIRIDGPIRLPIVDKYDMGTIVLKGLESIGIFKQQLVMMPNKHNVEVLGIL 347
Qy 536 NETENEVDMAWCGEQVKLRIRKGVBEEDIISPGFVLTSKPNPIKSVTKVAQIAIVELKSII 595
Db 348 SD-DTETDFVAPGENLKIRLKGIEEBEILPEFILCDPSNLCHSGRTDPDQIVIIIEHKSII 406
Qy 596 AAGFSCVMHVTATEEVHIVKLHLKLEKGTNRKSKPPAPFAKGMKVIAVLETEAPVCVE 655
Db 407 CPGYNAVLHIHTCIEEVEITALISLVDKSGEKSKTRPRFVKQDQVCIARLTAGTICLE 466
Qy 656 TYQDYPOLGRFTLRDQGTIIAIGKIVKI 683
Db 467 TFKDFPQWGRFTLRDEGKTTAIGKVLKL 494
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RESULT 7

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US-09-976-165-40
; Sequence 40, Application US/09976165
; Patent No. 6562947
; GENERAL INFORMATION:
; APPLICANT: FUJIWARA, TSUTOMU
; APPLICANT: WATANABE, TAKESHI
; APPLICANT: HORIE, MASATO
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
; FILE REFERENCE: Q-53599
; CURRENT APPLICATION NUMBER: US/09/976,165
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/565,538
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 09/055,699
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/820,170
; PRIOR FILING DATE: 1997-03-19
; PRIOR APPLICATION NUMBER: JP 63410/1996
; PRIOR FILING DATE: 1996-03-19
; PRIOR APPLICATION NUMBER: JP 69163/1997
; PRIOR FILING DATE: 1997-03-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-976-165-40
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Query Match 36.4%; Score 1307.5; DB 4; Length 499;
Best Local Similarity 49.4%; Pred. No. 3.1e-106;
Matches 251; Conservative 94; Mismatches 146; Indels 17; Gaps 5;
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Qy 178 ETKEPTKEPTKVEBPVKKEEKPVQTEKTEKSELKPVEDLKISESTHNTNNAVTSADA 237
Db 2 ELSEPVEVEGE-----MALESWEHSKEVSEAEPP---GGSGSDSGPPEESQGE 49
Qy 238 LIKEQEE--EVDDEVNDMFGKDHVSLIFMGHVDAGKSTMGGNLLYLTGSDVKRTIEKY 295
Db 50 MMEKEEIRKSKSVIVPSGAPKKEHVNVFVIGHVDAGKSTIGGIMFLTGMADKRTIEKY 109
Qy 296 EREKADAGROGWYLSWMDTNKEERNDGKTIEVGKAYFETEKRRYTTILDAPGHKMYVSEM 355
Db 110 EREAENKRETWYLSWALDNTQBERDKGKTVEUGRAYFETERKHFTTILDAPGHKSFVPNM 169
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Qy 356 IGGASQADVGLVISARKGEYETGPERGGOTREHALLAKTOGVNKNVWVVKMDDPTVNW 415
Db 170 IGGASQADLVLVISARKGEFEETFEKGGQREHAMFGKTAGVXHLIVLKNKDDPTVNW 229
Qy 416 SKERYDOCVSNVSNPLRAIGNIKITDVVFMVPSVSGYSGANLKHVDPKCEPWTGTLLLEY 475
Db 230 GIEREYBECKLVFLKVKVSPKDIHFMCISGLTGANIKEQSD--FCPWYTGLPFPY 287
Qy 476 LDTWNHVDHINAPFMLPIAAKMDLGTIVGKIESGHKKGQSTLMPNKTAVEIQNIY 535
Db 288 LNNLPNFRNSIDGPIRLPVDKYDMGTIVLKGLESIGFQGOQVLMNPNKHNEVLGIL 347
Qy 536 NETENEVDAMCGOVKLRIGKVEEEDISPGFVLTSKPNPKSVTKFVAQIAIIVELKSI 595
Db 348 SD-TDETFDVAAGBNLIRLKGIBEEILPEFILCDPSNLCHSGRTEDVQIVIEHKSII 406
Qy 596 AAGFSCVMHVTAEIEVHIVKLLHLEKGTNRKSKPPAFKGMKVIAVLETEAPVCVE 655
Db 407 CPGINAVLHIHTCEEVEITALISIVDKKSEKSTRPRFVKQDOVCIARLRTAGTICLE 466
Qy 656 TYQDYPOLGRFTLRDQGTIIAGKIVKI 683
Db 467 TFKDFPQMGRTLRDEGTIIAGKIVKL 494
RESULT 8
US-09-248-796A-19828
; Sequence 19828, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19828
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19828
Query Match 29.8%; Score 1072.5; DB 4; Length 276;
Best Local Similarity 70.3%; Pred. No. 5.7e-86;
Matches 194; Conservative 40; Mismatches 41; Indels 1; Gaps 1;
Qy 408 MDDPTVWNSKERYDQCVSNVSNFLRAIGNIKITDVWPMVPSVSGYSGANLKHVDPKCEPWI 467
Db 1 MDDSTVWNSKERYDQCVSNVSNFLRAIGNIKITDVWPMVPSVSGYSGANLKHVDPKCEPWI 59
Qy 468 TGPTLLBYLDTMNHVDHINAPFMLPIAAKMDLGTIVGKIESGHKKGQSTLMPNKT 527
Db 60 DGPSLLEYLDNMDTMNRKINGPFPMPVSGMKDLGTIVGKIESGHKKGQSTLMPNKT 119
Qy 528 AVEIQNIYNETENEVDAMCGEYKLRIGKVEEEDISPGFVLTSKPNPKSVTKFVAQIA 587
Db 120 PIEVLITFNETEQEDTAFSGEYKLRIGKVEEEDISPGFVLTSKPNPKSVTKFVAQIA 179
Qy 588 IVELKSIIAAGFSCVMHVTAEIEVHIVKLLHLEKGTNRKSKPPAFKGMKVIAVLE 647
Db 180 IVELKSIILNSGFCVMHVTAEIEVHIVKLLHLEKGTNRKSKPPAFKGMKVIAVLE 239
Qy 648 TEAPVCVETYQDYPQLGRFTLRDQGTIIAGKIVKI 683
Db 240 VGLVCAETYQDYPQLGRFTLRDQGTIIAGKIVKL 275
RESULT 9

US-09-248-796A-19819
; Sequence 19819, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19819
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19819
Query Match 23.1%; Score 831; DB 4; Length 460;
Best Local Similarity 39.0%; Pred. No. 2.3e-64;
Matches 173; Conservative 87; Mismatches 160; Indels 24; Gaps 9;
Qy 258 KDHVSLIFPMGHVDAGKSTMGNNLLYLTGSDVKRTIEKYEREAKDAGROGWYLSWVMDTNK 317
Db 7 KTHVNVVIVGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKAABLKGSPFYAWVLDKLG 66
Qy 318 EERNDGKTIIEVGKAYFETEKRRYTLDPAGHKMYSSEMIGGASOADVGLVISARKGEYE 377
Db 67 AERERGITIDIALWKFPETPKYHTVVIDAPGHRDFIKNMITGTSQADCAILLIAGTGGEFE 126
Qy 378 TGFERGGQTRHALLAKTOGVNKNVWVVKMDDPTVWNSKERYDQCVSNVSNFLRAIGNY 437
Db 127 AGTSKQGTREHALLAYTLGVKQLIVAVNKM--SVKMDKRFEEIKETSNFVKKVCYN 184
Qy 438 IKTDVPMVPSVSGYSGANLKHVDPK-ECPWY-----TGPTLLBYLDTMNHVDR 484
Db 185 PKT-VFPVPIISGWNDDN--IEPSTNCPWYKGEKETKSGKVTGKTILLEAIDAIEPPT 240
Qy 485 HINAPFMLPI--AAKMDLGTIVGKIESGHKKGQSTLMPNKTAVEIQNIYNETENEV 542
Db 241 PTDKPLRLPLQDVYKIGGIGTVPGRVETGIIKAGMVVTFAPAGVTEKSVEMHHE--QL 299
Qy 543 DMAMCGEQVKLRIGKVEEEDISPGFVLTSKPN-PIKSVTKFVAQIAIIVELKSIIAAGFSC 601
Db 300 AEGVPGDVGNGVSNVSKIRRGVNCVCGDSKNDPPKGCDSFNAQVIVLNHPQISAGYSP 359
Qy 602 VMHVHTAIEVHIVKLLHLEKGTNRKSKPPAFKGMKVIAVLETEAPVCVETYQDYP 661
Db 360 VLDCHTAHIAKCFDTLVEKIDRRTGKLEENPKFVSGDAAIIVKVPPTKPCVBEAFTDYP 419
Qy 662 QLGRFTLRDQGTIIAGKIVKIAE 685
Db 420 PLGRFAVRDMRQTVAVG-VIKSVE 442
RESULT 10
US-08-299-351-1
; Sequence 1, Application US/08299351
; Patent No. 5576186
; GENERAL INFORMATION:
; APPLICANT: Stetler, Dean A.
; TITLE OF INVENTION: DIAGNOSIS AND MONITORING OF
; TITLE OF INVENTION: RHEUMATOLOGICAL DISEASES BY DETECTION OF ANTI-EP-1alpha
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 1400 Mercantile Bank Tower, 1101 Walnut St.
; CITY: Kansas City
; STATE: Missouri


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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9570
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9570

Query Match      22.2%; Score 797.5; DB 4; Length 469;
Best Local Similarity 38.5%; Pred. No. 2.1e-61;
Matches 170; Conservative 88; Mismatches 158; Indels 25; Gaps 8;

Qy 258 KDHSVLPFMGHVDAGKSTMGNNLLYLTGSDVKRTIEKYERAKDAGROGWLSWYMDTNK 317
Db 12 KTHNIVVIGHVDSKSTTTGHLIYKCGGIDKRTIEKEKAEMGKSPKYAWVLDKLG 71

Qy 318 ERNDGKTIEVGKAYFETEKERYTILDAPGHMYSVEMIGGASQADVGVLVISARKGEYE 377
Db 72 AERERGITIDISLWKFTSKYVVTIIDAPGHRDFIKNMITGTSQADCAVLIVAAGVGGE 131

Qy 378 TGFERGGOTREHALLAKTQGVNKMVVVNMKDDPTVNMKERYDYOCVSNVSNFLRAIGN 437
Db 132 AGISKNGOTREHALLAYTLGVKQLIVGNKMDSTPPYSQRYEIEVKEVSYIKKIGYN 191

Qy 438 IKTDVFMFVPSVSGYSGANLKHVDPK-ECPMY-----TGPTLLEYLDTMNHVDR 484
Db 192 PDT-VAFPVPSGNGDNM--LEPSANMPWFKGMKVKTRKDGNASGTTILLEALDCLPPT 247

Qy 485 HINAPFMLPI--AAKMDLGTIVGKIESGHIKKGQSTLLMPNKTAVBIONI--YNETEN 540
Db 248 PTDKPLRLPLQDVYKIGGIGTVPVGRVETGLKPGMVVTFAPVNVVTTTEVKSVMHEALS 307

Qy 541 EVDNMGCEQVKLRKIGVEEEDISPGFVLTSPKN-PIKSVTKFVAQIAIVELKSLIAAGF 599
Db 308 E---ALPGDNVGFNVKNSVDRGNVAGSKNDPPMEAAAGFTAQVILNHPGQISAGY 364

Qy 600 SCVHVHTAIEBHIVKLLHLEKGTNRKSKPPAFKKGKMKVIAVLETEAPVCVETTYQD 659
Db 365 APVLDCHTAHTACKFAELKEKIDRRSGKLEDGPKFLKSGDAAIVDMVPGKPMCVESFSD 424

Qy 660 YPOLGRFTLRDQGTIIAGKI 680
Db 425 YPPLGRFAVRDMQTAVGV 445

RESULT 13
US-09-949-016-9571
; Sequence 9571, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9571
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9571
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Query Match      22.2%; Score 797.5; DB 4; Length 469;
Best Local Similarity 38.5%; Pred. No. 2.1e-61;
Matches 170; Conservative 88; Mismatches 158; Indels 25; Gaps 8;

Qy 258 KDHSVLPFMGHVDAGKSTMGNNLLYLTGSDVKRTIEKYERAKDAGROGWLSWYMDTNK 317
Db 12 KTHNIVVIGHVDSKSTTTGHLIYKCGGIDKRTIEKEKAEMGKSPKYAWVLDKLG 71

Qy 318 ERNDGKTIEVGKAYFETEKERYTILDAPGHMYSVEMIGGASQADVGVLVISARKGEYE 377
Db 72 AERERGITIDISLWKFTSKYVVTIIDAPGHRDFIKNMITGTSQADCAVLIVAAGVGGE 131

Qy 378 TGFERGGOTREHALLAKTQGVNKMVVVNMKDDPTVNMKERYDYOCVSNVSNFLRAIGN 437
Db 132 AGISKNGOTREHALLAYTLGVKQLIVGNKMDSTPPYSQRYEIEVKEVSYIKKIGYN 191

Qy 438 IKTDVFMFVPSVSGYSGANLKHVDPK-ECPMY-----TGPTLLEYLDTMNHVDR 484
Db 192 PDT-VAFPVPSGNGDNM--LEPSANMPWFKGMKVKTRKDGNASGTTILLEALDCLPPT 247

Qy 485 HINAPFMLPI--AAKMDLGTIVGKIESGHIKKGQSTLLMPNKTAVBIONI--YNETEN 540
Db 248 PTDKPLRLPLQDVYKIGGIGTVPVGRVETGLKPGMVVTFAPVNVVTTTEVKSVMHEALS 307

Qy 541 EVDNMGCEQVKLRKIGVEEEDISPGFVLTSPKN-PIKSVTKFVAQIAIVELKSLIAAGF 599
Db 308 E---ALPGDNVGFNVKNSVDRGNVAGSKNDPPMEAAAGFTAQVILNHPGQISAGY 364

Qy 600 SCVHVHTAIEBHIVKLLHLEKGTNRKSKPPAFKKGKMKVIAVLETEAPVCVETTYQD 659
Db 365 APVLDCHTAHTACKFAELKEKIDRRSGKLEDGPKFLKSGDAAIVDMVPGKPMCVESFSD 424

Qy 660 YPOLGRFTLRDQGTIIAGKI 680
Db 425 YPPLGRFAVRDMQTAVGV 445

RESULT 14
US-09-309-572-10
; Sequence 10, Application US/09309572
; Patent No. 6440730
; GENERAL INFORMATION:
; APPLICANT: Heinrich-Pette-Institut
; TITLE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV
; FILE REFERENCE: P50489
; CURRENT APPLICATION NUMBER: US/09/309,572
; CURRENT FILING DATE: 1999-05-11
; EARLIER APPLICATION NUMBER: DE 198 56 463
; EARLIER FILING DATE: 1998-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: elongation factor EF-1-alpha
US-09-309-572-10

Query Match      22.2%; Score 796.5; DB 4; Length 462;
Best Local Similarity 38.3%; Pred. No. 2.5e-61;
Matches 169; Conservative 89; Mismatches 158; Indels 25; Gaps 8;

Qy 258 KDHSVLPFMGHVDAGKSTMGNNLLYLTGSDVKRTIEKYERAKDAGROGWLSWYMDTNK 317
Db 5 KTHNIVVIGHVDSKSTTTGHLIYKCGGIDKRTIEKEKAEMGKSPKYAWVLDKLG 64

Qy 318 ERNDGKTIEVGKAYFETEKERYTILDAPGHMYSVEMIGGASQADVGVLVISARKGEYE 377
Db 65 AERERGITIDISLWKFTSKYVVTIIDAPGHRDFIKNMITGTSQADCAVLIVAAGVGGE 124

Qy 378 TGFERGGOTREHALLAKTQGVNKMVVVNMKDDPTVNMKERYDYOCVSNVSNFLRAIGN 437
Db 132 AGISKNGOTREHALLAYTLGVKQLIVGNKMDSTPPYSQRYEIEVKEVSYIKKIGYN 191
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Db 125 AGISKNGQTRHALLAVTLGVKQLIVGNKMDSTPPYSQRYBEIVKEVSTYIKKIGYN 184
Qy 438 IKTDVFMPSGYSGANLKOHVDPK-ECPLY------TGPTLLEYLDTMNHVDR 484
Db 185 PDT-VAFVPISGWNGDNM---LEPSANMPFKGWKVTNRKDGNSGTTLLLEALDCILPPT 240
Qy 485 HINAPFMLPI--AAKMDLGTIVRGKIESGHIKKQSTLLMPNKTAVEIQNI--YNETEN 540
Db 241 PTDKPLRLPLQDVYKIGIGITVPGRVETGVLKPGMVVTFAPVNVVTEVKSVEVHHEALS 300
Qy 541 EVDWAMCGEQVKLRKIGVEEBDISPGFVLTSPPKN-PIKSVTKFVAQIAIIVELKSIIAAGF 599
Db 301 E---ALPGDNVGNVKNVSKDVRGNAVAGDSKNDPPMEAAGFTAQVVIILNHPQISAGY 357
Qy 600 SCVMHVHTAIEEVHIVKLLHLEKGTNRKSKPPAPAKKGMKVIAVLETAAPVCVETYQD 659
Db 358 APVLDCHTAHIAKFAELKEKIDRRSGKLEDPKFLKSGDAAIVDMVPGKPMCVESFSD 417
Qy 660 YPOLGRFTLRDQGTITIAIGKI 680
Db 418 YPPLGRFAVRDMRQTVAVGVI 438

RESULT 15

US-09-718-096-10
; Sequence 10, Application US/09718096
; Patent No. 6589763
; GENERAL INFORMATION:
; APPLICANT: Von Laer, Meike-Dorothee
; TITLE OF INVENTION: RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH LCMV
; FILE REFERENCE: 35-195
; CURRENT APPLICATION NUMBER: US/09/718,096
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: DE 19856463.5
; PRIOR FILING DATE: 1998-11-26
; PRIOR APPLICATION NUMBER: EP 99250415.9
; PRIOR FILING DATE: 1999-11-25
; PRIOR APPLICATION NUMBER: US 09/309,572
; PRIOR FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: elongation factor EF-1-alpha
US-09-718-096-10

Query Match 22.2%; Score 796.5; DB 4; Length 462;
Best Local Similarity 38.3%; Pred. No. 2.5e-61;
Matches 169; Conservative 89; Mismatches 158; Indels 25; Gaps 8;
Qy 258 KDHVSLIFMGHVDAGKSTMGNLLYLTGSDVKRTIEKYERAKDAGRGWYLSWVMDTNK 317
Db 5 KTHINIVVIGHVDGSKSTTGHLYKCGIDKRTIEKEAEAKGSGFKYAWVLDKX 64
Qy 318 EERNKGKTIIEVGKAYFETEKERYTILDPAGHKMVTSEMIGGASQADVGLVISARKGEYE 377
Db 65 AERERGITIDISLWKFTSKYVVTIIDAPGHRDFIKNMITGTSQADCAVLIVAAAGVGEFE 124
Qy 378 TGPERGGQTRHALLAKTQGNKMWVNMDDPTVWNSKERYDCVSNFSLRAIGYN 437
Db 125 AGISKNGQTRHALLAVTLGVKQLIVGNKMDSTPPYSQRYBEIVKEVSTYIKKIGYN 184
Qy 438 IKTDVFMPSGYSGANLKOHVDPK-ECPLY------TGPTLLEYLDTMNHVDR 484
Db 185 PDT-VAFVPISGWNGDNM---LEPSANMPFKGWKVTNRKDGNSGTTLLLEALDCILPPT 240
Qy 485 HINAPFMLPI--AAKMDLGTIVRGKIESGHIKKQSTLLMPNKTAVEIQNI--YNETEN 540
Db 241 PTDKPLRLPLQDVYKIGIGITVPGRVETGVLKPGMVVTFAPVNVVTEVKSVEVHHEALS 300

Qy 541 EVDWAMCGEQVKLRKIGVEEBDISPGFVLTSPPKN-PIKSVTKFVAQIAIIVELKSIIAAGF 599
Db 301 E---ALPGDNVGNVKNVSKDVRGNAVAGDSKNDPPMEAAGFTAQVVIILNHPQISAGY 357
Qy 600 SCVMHVHTAIEEVHIVKLLHLEKGTNRKSKPPAPAKKGMKVIAVLETAAPVCVETYQD 659
Db 358 APVLDCHTAHIAKFAELKEKIDRRSGKLEDPKFLKSGDAAIVDMVPGKPMCVESFSD 417
Qy 660 YPOLGRFTLRDQGTITIAIGKI 680
Db 418 YPPLGRFAVRDMRQTVAVGVI 438

Search completed: July 1, 2005, 18:39:39
Job time : 58.3582 secs

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OM protein - protein search, using sw model

Run on: July 1, 2005, 18:20:02 ; Search time 180.127 Seconds
(without alignments)
1467.128 Million cell updates

US-09-591-632-2

Perfect score: 3594
Sequence: 1 MSDSNQNNQNYQYQSQNG.....FTLRDQGTITAIKIVKIAE 685

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1722976 seqs, 385795295 residues

Total number of hits satisfying chosen parameters: 1722976

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

```

Database : Published Applications AA:**
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pcp:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pcp:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pcp:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pcp:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pcp:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pcp:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pcp:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pcp:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pcp:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pcp:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pcp:*
16: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pcp:*
17: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pcp:*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pcp:*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pcp:*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pcp:*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pcp:*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pcp:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	2549.5	70.9	662	17	US-10-732-923-17478	Sequence 17478, A	
2	2367	65.9	712	17	US-10-732-923-17486	Sequence 17486, A	
3	2347.5	65.3	721	14	US-10-032-585-7274	Sequence 7274, Ap	
4	2283.5	63.5	701	17	US-10-732-923-17479	Sequence 17479, A	
5	2177	60.6	741	17	US-10-732-923-17107	Sequence 17107, A	
6	1877	52.2	742	17	US-10-732-923-17477	Sequence 17477, A	
7	1679.5	46.7	690	15	US-10-369-493-22730	Sequence 22730, A	
8	1658	46.1	720	15	US-10-320-797-3284	Sequence 3284, Ap	
9	1626	45.2	629	17	US-10-732-923-17101	Sequence 17101, A	
10	1557.5	43.3	716	14	US-10-128-714-8108	Sequence 8108, Ap	
11	1519.5	42.3	712	14	US-10-128-714-3108	Sequence 3108, Ap	

12	1364.5	38.0	634	15	US-10-108-260A-3174	Sequence 3174, A
13	1354.5	37.7	499	14	US-10-146-473-46	Sequence 46, Appl
14	1354.5	37.7	499	16	US-10-788-792-231	Sequence 231, App
15	1338.5	37.2	533	15	US-10-425-114-44453	Sequence 44453, A
16	1337.5	36.4	499	9	US-09-976-165-40	Sequence 40, Appl
17	1307.5	36.4	499	14	US-10-342-276-40	Sequence 40, Appl
18	1283.5	35.7	515	17	US-10-732-923-17097	Sequence 17097, A
19	1238	34.4	505	15	US-10-424-599-210116	Sequence 210116, A
20	1211.5	34.0	531	16	US-10-437-963-189003	Sequence 189003, A
21	1149	32.0	409	15	US-10-424-593-17528	Sequence 17528, A
22	1086	30.2	587	17	US-10-732-923-17528	Sequence 17528, A
23	1030.5	28.7	805	17	US-10-732-923-17528	Sequence 17528, A
24	1009	28.1	389	16	US-10-437-963-191100	Sequence 191100, A
25	943	26.2	600	17	US-10-732-923-17126	Sequence 17126, A
26	926.5	25.8	682	17	US-10-732-923-17127	Sequence 17127, A
27	922.5	25.7	684	17	US-10-732-923-17780	Sequence 17800, A
28	912	25.4	496	17	US-10-732-923-17789	Sequence 17789, A
29	897	25.0	652	17	US-10-732-923-17363	Sequence 17363, A
30	859.5	23.9	435	17	US-10-732-923-17119	Sequence 17119, A
31	848	23.6	653	17	US-10-732-923-17692	Sequence 17692, A
32	844	23.5	450	17	US-10-732-923-17450	Sequence 17450, A
33	844	23.5	453	17	US-10-732-923-17449	Sequence 17449, A
34	844	23.5	456	17	US-10-732-923-17451	Sequence 17451, A
35	842.5	23.4	451	17	US-10-732-923-17092	Sequence 17092, A
36	842	23.4	435	17	US-10-732-923-17086	Sequence 17086, A
37	838.5	23.3	449	17	US-10-732-923-17527	Sequence 17527, A
38	836.5	23.3	449	17	US-10-732-923-17523	Sequence 17523, A
39	829	23.1	458	17	US-10-732-923-17104	Sequence 17104, A
40	828.5	23.1	449	17	US-10-732-923-17525	Sequence 17525, A
41	828	23.0	461	17	US-10-732-923-17093	Sequence 17093, A
42	827.5	23.0	461	17	US-10-732-923-17102	Sequence 17102, A
43	826.5	23.0	434	17	US-10-732-923-17228	Sequence 17228, A
44	825.5	23.0	460	17	US-10-732-923-17111	Sequence 17111, A
45	825	23.0	458	17	US-10-732-923-17103	Sequence 17103, A

ALIGNMENTS

```

RESULT 1
US-10-732-923-17478
; Sequence 17478, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE NUMBER: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 17478
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Zygosaccharomyces rouxii
US-10-732-923-17478

```

Query Match 70.9%; Score 2549.5; DB 17; Length 662;
Best Local Similarity 74.0%; Pred. No. 4.7e-157;
Matches 512; Conservative 53; Mismatches 90; Indels 37; Gaps 15;

1	MSDSNQGNQNYQYQYSONGNOQGNRYYQY-QAYNAQAQAPAGGYQNTQYGSYGOQGG	59	QY
1	MSDPNQ-NGQ-----QGGQNAAGNYQYQYFQKLTAQAQ-AGGGYQPYGGYGY--GG	49	Db
60	YQYNNPDAGYQOQYNNPQGGYQ-QYNPQGGYQOQFNPOGGRGNYNKFNNNNLQYQAGFQ	118	QY
50	YGGYQPYGYYQOYF--QDQQAQAGYNGYPYQ--AQCAPEGFN--NYYNQFQP-----Q	98	Db
119	POSQMSLNDFOKQQ---KQAAPKPKTKTLKLVSSSGIKLANATKKVGTQPAESDKKEEK	175	QY
99	QOSQGWTLDDFHKKOTQSAPPKQKSLKLVSSSGIKLANATK---KPKBEKKEKEEP	154	Db


```
Best Local Similarity 48.4%; Pred. No. 4.2e-97;
Matches 310; Conservative 134; Mismatches 117; Indels 80; Gaps 14;

Qy 71 QQYNPOGGYQOYNPOG-----GQQQFNPOGGRGNTK--NFNNY---N 109
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 37 EEFPRNMY--YGFQDCTMNCANMYPGHFMGYNQRYDDR---KYPCNRDYSRQGMN 90
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 110 LOGVOAGF-QPOSGMSLNDFOKQKQAAKPKKTKLKLVSSSGIKLANATKKVGTKAES 168
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 91 IRGIEKMTTPESKG-----SATSGQRT-----SAKVJRVDADPKVSLDGSVV 134
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 169 DKKEEESAETKEPTKVVEEPVKKEEPVQTEETKEKSELPKVEDLKISESTHTN 228
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 135 GRNGNR-----VNKVDKRVPSMD-----MENLSLAASKQKKN 166
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 229 NANVTSADA-----LIKEEBEVDVNDMFGKHVSLIFMGHVDAGKSTMGNNLLYL 283
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 167 HVSVTGDEERKDLIASQFOEIDEVLQDIY-GKEHNVVVFIGHVDAGKSTLGGNLYM 225
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 284 TGSVDKETIEKYEREAKDAGRGWYLSVMWDTNKEERNDGKTIHVGRAYETEKRRYIIL 343
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 226 TGMVDKTMETKYEKDAKEAGRESWYLSWALDSTKEERSKGTIVLGRAYETEKRRYIIL 285
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 344 DAPGHKMYVSEMIIGGASQADYGLVVISARKGEYETGFERGGQTRHALLAKTQGVNPOVV 403
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 286 DAPGHKSYVPMIBGTAQAEVAVLVISARKGEYETGFERGGQTRHALLAKTQGVSKLIV 345
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 404 VVNMKDDPTVNSKERYDQCQSVNSVNFRL-AIGNIKITDVVFMVPSVSGANLKDHDVDPK 462
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 346 AINRMKDDPTVNSKERYDECTNGITTFRLKEVGYNPKTDFVFMPISAFTGINIKERIDKK 405
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 463 ECPMYTGPTLLVLDTMNHVDRHINAPFMLPIAAKMDLGTIVGKTESGHIKKGQSTLL 522
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 406 ICPWYNGPSLLEYLDEMDFTERKUNTPLIPIQAKYKDMGLVIBGKIESGTVFKGNSVIL 465
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 523 MPNKTAVEIQIYNETENEVDMAECGEQVKLRIRKGVVEEDISPGFVLTSKPNPIKSVTKF 582
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 466 MPNKTVVVVGLYNELE-EIRVGRCGQIKLRIRKGVVEEDVMTGHILLSLESVPSTAKIF 524
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 583 VAQIAVELKSIIAAGSCVMHVTAEVHVIVKLLHLEKGTNRKSKKPPAPAKKGMKV 642
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 525 EAQIAILEVSLLTAGYSCTIIHISAVQEVFTFLKLLYKLLDKLTNRKSKKPPAFATKGMKI 584
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 643 IAVLETEAPVCVETYQDYPOLGREFTLRDQGTIIAIGKIVKI 683
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 585 VALLEVASPLCLETFDYKIQLGRLRNEGLTVAGKVTKL 625
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
US-10-128-714-8108
; Sequence 8108, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wenqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroskin, Alexey M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
```

```
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8108
; LENGTH: 716
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-8108

Query Match 43.3%; Score 1557.5; DB 14; Length 716;
Best Local Similarity 46.6%; Pred. No. 1.4e-92;
Matches 332; Conservative 99; Mismatches 186; Indels 95; Gaps 18;

Qy 11 QNYQOYSQNGNQCGNNRQYQAYNAQAOPAGGYQNYQYSGYQOQGGYQOYNPDAGYQ 70
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 55 QTQQYQ-GGYPOVG--QYGYFAYDQQQGGFGQY-----GAYAQQFEGYNQI---YN 101
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 71 QQYNPOGGYQOYNPOGGYQOQFNPOGGRGNYKNFNNNNLOGYOAGFQPOSGMSL---- 126
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 102 NQY---GGYNQHQ-----QQQYT-----QPPRQAAPVATQA 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 127 NDFQKQKQQAAPKPKT-----LKLVSSSGIKLANATK--KVGT--KPAESDKKEEKS 177
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 PSAPAQAQAPKAPKAPASTASAAAPVLSIGGASSSSAAAPKTVLSIGTPSPA-----S 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 178 ETKEPTKEPTKVVEEPVKKEEPVQTEETKEKSELPKVEDLKIS-----ESTH 225
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 180 NTFSGITTPGDTWGSAAADAAAKVATASKAJEKTAKAAASGKSSPTTASGRSSPGRSSP 239
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 226 NTNANVT--SADALIKEEBEVDVNDMFG-GKDHVSLIFMGHVDAGKSTMGNNLLY 282
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 240 SRGEGGKTGRDANAVALAQADVEETLKEIYGEKKEHNVIVFIGHVDAGKSTLGGSILY 299
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 283 LTGSVDKRTTEKYEREAKDAGRGWYLSVMWDTNKEERNDGKTIHVGRAYETEKRRYIIL 336
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 300 VTGNVDERTLEKYKREAKEAGRETWYLSWALDLTNEERAKGKTVEVGRGHFKLTVQSPDG 359
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 337 --KRRYVITLDPAGHKMYVSEMIIGGASQADYGLVVISARKGEYETGFERGGQTRHALLAK 394
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 360 PIEHFSLIDAPGHKSYVHMIIGGASQADYGLVVISARKGEYETGFERGGQTRHALLAR 419
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 395 TQGVNKMVVVNMKDDPTVNSKERYDQCQSVNSVNFRLAIGNIKITDVVFMVPSVSGYSGAN 454
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 420 NTGVKKIIVAVNMKDDPTVNSKERYDQCQSVNSVNFRLAIGNIKITDVVFMVPSVSGYSGAN 478
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 455 LKHVDPKCEPWTGPTLLILEYLDTMNHVDRHINAPFMLPIAAKMDLGTIVGKTESGHI 514
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 479 IKDRVPKELAPWYNGPSLLEYLAEMKTPERNINAPFMPVSTKYRDMGTWVEGRIEAGVI 538
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 515 KKGOSTLLMPNKTAVEIQIYNETENEVDMAECGEQVKLRIRKGVVEEDISPGFVLTSKPN 574
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 539 KQATCTIMPNRYKVEIAALYGETEDELATATCGDYVRMLRGVVEEDLLPGFVLCSPKR 598
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 575 PIKSVTKFVAQIAVELKSIIAAGSCVMHVTAEVHVIVKLLHLEKGTNRKSKKPPA 634
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 599 LVHCVSFAEKIRILELKNILTACYNVCMHVSABEETFAALLHKCEKPGTGRSKRPPPP 658
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 635 PAKKGMKIVIA---VLETEAPVCVETYQDYPOLGREFTLRDQGTIIAIGKIVKI 683
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 659 FASKGQTIIRLEVISSAGVAVCVFERFEDYNQMGRTFLRDQGTIIAIGMITKL 710
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-10-128-714-3108
; Sequence 3108, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wenqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroskin, Alexey M
; APPLICANT: Lemieux, Sebastien
```


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